Thu Oct 23 06:05:19 2003

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GenCore version 5.1.6
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OM nucleic - nuc	OM nucleic - nucleic search, using sw model
Run on:	October 22, 2003, 17:13:34 ; Search time 7709 Seconds (without alignments) 11414.789 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-601-168B-1 2151 1 tgcgttgggttgggcttggcgttttgccagaaaaaaaa 2151
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	2888711 segs, 20454813386 residues
rotal number of	Total number of hits satisfying chosen parameters: 5777422
Minimum DB seq length: 0	length: 0 length: 200000000
Post-processing:	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Jatabase :	GenEmbl:* 1: gb_ba:* 2: gb_htg:*

99 htg: \*
90 ow: \*
90 ow: \*
90 ov: \*
90 pt: \*
90 vi: \*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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FEATURES source CDS	BASE COUNT ORIGIN Query Match Best Local Matches 215 Qy 1	·	, a & a & a

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TITLE Human beta TrCP protein	Query Match         100.0%;         Score 2151;         DB 6;         Length 2151;           Best Local Similarity 100.0%;         Pred. No. 0;         0. 0;         0;         Gaps         0;           Matches 2151;         Conservative 0;         Mismatches 0;         1 ndc1         0;         Gaps 0;           Qy         1 ndcGTndGCTGGGCCTGGCACCAAAGGGGCCCCGGGGAGAGCGGACCCAGTGGCC 0         1 ndcGTnGGCTGCGCCTGGCACCAAAAGGGGCCCCGGGGGAGAGCGGACCCAGTGGCC 0	QY         61 TCGGCGATTATGGACCCGGCGGGGGGGTGCTGCAAGAGAAGACACTCAAGTTTATGAAT 120           Db         61 TCGGCGATTATGGACCCGGCCGAGGCGGTGCTGCAAGAGAGATTATGAAT 120           QY         121 TCCTCAGAGAGAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATACCAGAGAAG 180           Db         121 TCCTCAGAGAGAGACTGTAATAATAGCGAACCCCCTAGGAAGATAATACCAGAGAAG 180	QY         181 AATTCACTTAGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAAGAACAGTA 240           Db         181 AATTCACTTAGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAGAAACAGTA 240           QY         241 TGTTTAGCAAGCACTGCTAGAAGACTGAGAAATTGTGGGCCAAAACAAAACAAAT 300           Db         241 TGTTTAGCAAGCACTGCTATGAAGACTGAGAAATTGTGTGGCCAAAACTTGCCAAT 300	OY 301 GGCACTTCCAGTATGTGCCCAAGCAACGGAAACTCTCAGCAAGGTATGAAAAGGAA 360  Db 301 GGCACTTCCAGTATGATTGTGCCCAAGCAAGCAAACTCTCAGCAAGCTATGAAAAGGAA 360	QY         361 AAGGAACTGTGTGTCAAATACTTTGAGCAGTGGACTCAGATCAGTGGAATTTGTG         420           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
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2151 bp mRNA linear PRI 31-OCT-1999
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/function="regulates the stability of IkappaB alpha- and
beta-catenin"
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Cenciarelli,C., Chiaur,D.S., Guardavaccaro,D., Parks,W., Vidal,M. and Pagano,M.
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                                                                                              CGTTCCCCTTCTCGAACATACACCTACACCATAAATAACCATACACTAACCATA
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Direct Submission
Direct Submission
Submitted (19.2 FB-1999) Pathology, NYU Medical Center, 550
Ave. MSB 548, New York, NY 10016, USA
Location/Qualifiers
1. .2151
/ organism="Homo sapiens"
/ mol_type="mRNA"
/ db xref="taxon:9606"
/ map="10924"
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/codon_start=1
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WRFPDGWAPPNSFYRALYPKIIQDIETIESNWRCGRHSLORIHGSETSKGYYCLQYD
DQKLVSGLRDWIIKIWDKWTNIECKRILTGHTGSVLCLQVDBEWVIITGSSDSTVRYWDV
NYGBWLWTLIHGERALLHLERWGMWYTCSKORSIAWDMASPTDITLRRULVGHRAA
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Homo sapiens mRNA for beta-transducin repeat containing protein.
Y14153
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Margottin,F., Bour,S.P., Durand,H., Selig,L., Benichou,S., Richard,V., Thomas,D., Strebel,K. and Benazous,R.
A novel human WD protein, h.beta TrCp, that interacts with HIV-1 Vpu connects CD4 to the ER degradation pathway through an F-box
AACAACAGTAACAATCAAACTACTGCCCAGTTTCCCTGGACTAGCCGAGGAGCAGGGCTT
                              AACAACAGTAACAATCAAACTACTGCCCAGTTTCCCTGGACTAGCCGAGGAGCAGGGCTT
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beta-transducin repeats; beta-TRCP gene; WD repeat.
Homo sapiens (human)
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/mol_type="mRRA"
db xref="taxon:966"
/cell_line="Jurkat T-cell"
/cell_type="T lymphocyte"
lissue type="lymphoid"
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Submitted (03-JUL-1997) R. Benarous,
Interactions Proteiques, CHU Cochin,
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TTCAATAATGGCATGATGGTGACCTGCTCCCAAGGTCGTTCCATTGCTGTATGGGATATG GCCTCCCCAACTGACATTACCCTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGTCAAT TGTTTGCAGTACAGGGACAGGCTAGTAGTGAGTGGCTCATCTGACAACACTATCAGATTA TGGGACATAGAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGT TGTATTCGATTTGATAACAAGAGGATAGTCAGTGGGGGCCTATGATGGAAAAATTAAAGTG TGTATTCGATTTGATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAATTAAAGTG TGGGATCTTGTGGCTGTTGGACCCCCGTGCTCCTGCAGGACACTCTGTCTACGGACC TGGGATCTTGTGGCTGCTTGCTTTGGACCCCCGTGCTCCTGCAGGGACACTCTGTCTACGGACC TGGGACATAGAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGT AGGATGAGCAACAACAATCAAACTACTGCCCAGTTTCCCTGGACTAGCCGAGGA TGTTTGCAGTACAGGGACAGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTA 

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	RESULT 7 AF081887 LOCUS LOCUS LOCUS DEFINITION Mus musculus ubiquitin ligase FWD1 mRNA, complete cds. VERSION AF081887.1 GI:4336326 KEYWORDS KEYWOR			FEATURES Location/Qualifiers  source 1. 2175  / Organism="Mus musculus" / mol type="mRNA" / db xref="taxon:10090"  CDS 91. 1:800 / note="similar to beta-transducin repeat-containing protein TrcP; F-box protein; contains WD40 repeats"	/COGON_SETATE=1 //COGON_SETATE=1 //COGON_SETATE=1 //COGON_SETATE=1 //COGON_SETATE=1 //EXCRET=1 id="abjquitin ligase FWD1" //EXCRET=1 id="abjquitin ligase FWD1" //EXCRET=1 id="abjquitin ligase FWD1" //EXCRET=1 ion="WDPABAUCEKLIKFWNSEREDCNNGEPPRKIIPEKREKECTV //EXCRETSENDVERVERHELISOMCHYORGHINSTERPLORFITALPRACHDHINENI ISYLDAKSICAABLUCKEWYRYTESOMUMKKIISRWNFOSHURGLIAERGWGOYLEK NKPPDENAPPNSFYRALYPKIIODIETIESNWRCGRHSLORIHCRSETSKGVYCLOVD DOKT VSGLARDWTIKINDYSTLECKRIITGHTGSVCACLOVDRSDSTSTWWDV NAGEMUNTLIFHCEAVLHLRENGMYTTGHTGSVCACLOVDRSDSTSTWWDV NAGEMUNTLIFHCEAVLHLRENGMYTTGTSTRAWRGIACLOYRDRIAVSGSSDN TILMINIEGGACLREVEGHEELWRCIFFEDNRIISGANDGASADALDPRABA TILMINIEGGACLREVEGHEELWRCIFFEDNRIISGANDGANDASADEDCSCOGNYTV	ISR.  BASE COUNT 589 a 528 c 567 g 491 t  ORIGIN  Query Match  Rest Local Similarity 88.5%; Pred. No. 0;	vative TGCGGCCTGG

1 (bases 1 to 1818)
Yaron, A., Hatzubai, A., Davis, M., Lavon, I., Amit, S., Manning, A.M., Andersen, J.S., Mann, M., Mercurio, F. and Ben-Neriah, Y. Identification of the receptor component of the NappasBalpha-ubiquitin ligase
Nature 396 (6711), 590-594 (1998)

Eutheria, Primates, Catarrhini, Hominidae, Homo

Mammalia;

Mercurio, F., Mannig, A.M., Andersen, J.S.,

Hebrew University-Hadassah

Z (bases 1 to 1818)
Yaron, A., Hatzubai, A., Mercurio, F., Mann, M. and Ben-Neriah, Y.
Direct Submission
Submitted (27-00T-1998) Immunology, He Medical School, Jerusalem, Israel
Location/Qualifiers

9853396

1. .1818 /organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606"

<1. ... 1818 /note="beta-transducin

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445 g

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receptor component of IkappaBa-ubiquitin ligase; contains F-box and WD regions"

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CTTGCCAATGGCACTTCCAGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTAT
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21-JAN-1999 cds.

AF101784 linear PRI Homo sapiens b-TRCP variant B3RS-IkappaB mRNA, partial cAF101784 GI:4165135

RESULT 8
AF101784
LOCUS
DEFINITION

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Homo sapiens (human)

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

1612 CTTGTGGAGCATTCCGGAAGAGTTTTTCGACTACAGTTGATGAATTCCAGATTGTCAGT	RESULT 9 BC003989 BC003989 BC003989 BC003989 BC003989 BC003989 BC003989 BC003989 BC003899 BCC SOURCE MUS musculus (house mouse) ORGANISM BCC BCALPORTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Marmalia; Butheria; Roberta; Musculuse; Musculuse; Musculuse; Musculuse; REFERENCE Adminialia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Musculuse;		Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J.D., Butterfield,Y.S., Rarguez,A.C., Scrimwood,J., Samilus,D.E., Butterfield,Y.S., Krzywinski M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  MEDLINE 2388257  PUBMED 12477932  Chases I to 2081)  AUTHORS  Strausberg.R.  TITLE SLAMMission  JOURNAL Submitted (28 FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11403, Bethesda, MD 20892-2590,	USA  REMARK  NIH-MGC Project URL: http://mgc.nci.nih.gov  Contact: MGC help desk  Email: Ggabbs-r@mail.nih.gov  Tissue Procurement: Gilbert Smith. Ph.D.  CDNA Library Preparation: Life Technologies, Inc.  CDNA Library Preparation: Life Technologies, Inc.  CDNA Library Prayed by: The I.M.A.G.B. Consertium Genome  DNA Sequencing by: Sequencing Group at the Stanford Human Genome  Center, Stanford University School of Medicine, Stanford Human Genome  Center, Stanford University School of Medicine, Stanford, CA 94305  Web site: http://www-shgc.stanford.edu  Contact: (Dickson Mark) mad@paxil.stanford.edu  Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,  R. M.	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 8 Row: o Column: 21 This clone was selected for full length sequencing because it
TGCTGCTGAACTT 591  FIGCTGCTGAACTT 630  TGCTGCTGAACTT 630  CV AGAAGCTTATCGAG 651  FILLITITITITITITITITITITITITITITITITITIT	AGAGCA 771       AGAGCA 810 GGAAGA 831	GATAAA 990  CTCCAG 1011  CTCCAG 1050  GATGTA 1071  GATGTA 1110  TTGCGT 1131  TTGCGT 1170	3GGATATG 1191 3GGATATG 1230 CTGTCAAT 1251 [	3CATTGCC 1410 CCAGATTA 1431 CCAGATTA 1470 CGGGCGT 1491 CGGGGCGT 1530 CGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TGTCTACGGACC 1611
532 CATATCGCTGAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCT 571 CATATCGCTGAACAATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCT 572 CATATCGCTGAAGAACATTCTGTCATACCTGGATGCCAAATCACTATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	112 TATTATTCAAAACAAACCTCCTGAGGGAATGCTCCTCCCAACTCTTTTA.  751 TATTATTCAAAAACCAACCTCCTGAGGGAATGCTCCTCCCCAACTCTTTTA.  772 CTTTATCCTAAAATTATACAAGACATTGAGACAATGAATCTAATTGGAGATG.  811 CTTATCCTAAAATTATACAAGACATTGAGACAATGAATCTAATTGGAGATG.  822 CATAGTTACAAAAATTATACAAGAGAGAAACAAAGAACAAAGAATTACTG.  832 CATAGTTACAGAGAATTACTCCCGAAGTGAACAAGGAAAGAGTTACTG.  871 CATAGTTACAGAAAATAGTAAAGTGAAACAAACAAAGAATTACTG.	931 TATGATGATCAGAAATAGTAAGCGGCCTTCGAGACAACAATCAAGTCTGG 952 AACAATTGGAAATGGTAAGCGGCCTTCGAGACAACAATCAAGTCTGG 953 AACACATTGGAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCCTCTGT 1012 TATGATGAGAGTGATCATAACAGGATTCTCAGGGTTCAGGTTCAGTCCTCTGT 1051 TATGATGAGAGAGTGATCATAACAGGATCATCGGATTCCAGGTCAGGTGTGG 1052 TATGATGAGAGAGTGATCATAACAGGATCATCGAGTTCAGGTGTGG 1051 TATGATGAGAGAGTGATCATAACAGGATCATCGAGTTCAGGTTGGAGTTGGAGTTGGAGTTGGAGTTGGAGTTGGAGTTGGAGTTGGAGTTGGAGTTGGAGTTGGAGTTGGAGTTGGAGTTGGAGTTGCAGGTTGAACAGTTGAAACAGTTCAATTCACCATTGTGAAACAGGTTGAACAACAGTTCAATCACCATTGTGAAACAGGTTGAACAACAGTTCAACAACAGTTCAACAACAGTTCAACAACAGTTCAACAACAGTTCAACAACAGTTCAACAACAGTTCAACAACAACAGTTCAACAACAACAGTTCAACAACAACAAGTTCAACAACAAGTTCAACAACAAGTTCAACAACAACAAGTTCAACAACAACAAGTTCAACAACAACAAGTTCAACAACAACAAGTTCAACAACAACAACAAGTTCAACAACAACAAGTTCAACAACAACAAGTTCAACAACAACAAGTTCAACAACAACAACAATTCAACAACAACAACAACAACAA	12 TTCAATAATGGCATGATGGTGACCTGCTCCAAAGATCGTTCCATTG 11 TTCAATAATGGCATGATGGTGACCTGCTCCAAAGATCGTTCCATTG 12 GCCTCCCCAACTGACATTACCCTCCGGAGGTGCTGGTCGACGCTCCACTTG 13 GCCTCCCCAACTGACATTACCTTCGGAGGTGCTGGTCGGTC	TACTTGTGAATTTGTAAGGACCTTAAATGGACA CAGGGACAGGCTGGTAGTGAGTGGCTCATCTGAC CAGGGACAGGCTGGTAGTGGTGGCTCATCTGAC CAGGGACAGGTTACGAGTGGTTAGAAGGCCA ATGTGGTGCATGTTTACGAGTGTTAGAAGGCCA: ATGTGGTGCATGTTTACGAGTGTTAGAAGGCCA: TGATAACAAGGATAGTCAGTGGGGCCTATGA:	1552 IGGGAICTIGIGGCIGCTITGGACCCCCGIGCTCCTGCAGGGACACTCTGICIA 
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/clone lib="NCI CGAP_Lu29"
/lab_host="NetCGAP_Lu29"
/note="vector: pCMV-SPORT6"
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  following selection criteria: matched mRNA
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Winston, J., Elledge, S.J. and Harper, J.W.
Direct Submission
Submitted (01-DEC-1998) Biochemistry, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Location/Qualifiers
1.1979
                            TCCGGAAGAGTTTTTCGACTACAGTTTGATGAATTCCAGATTGTCAGTAGTTCACATGAT
                                              GACACAATCCTCATCTGGGACTTCCTAAATGATCCAGCTGCCCAAGCTGAACCCCCCGGT
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AFU99932 1712 bp mRNA linear ROD 21-JAN-1999
Mus musculus beta-TrCP protein E3RS-TkappaB mRNA, complete cds.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1712)
                                                                                                                                                                                     Yazon,A., Hatzubai,A., Davis,M., Lavon,I., Amit,S., Manning,A.M.,
Andersen,J.S., Mann,M., Mercurio,F. and Ben-Neriah,Y.
Identification of the receptor component of the
IkappaBalpha-ubiquitin ligase
Nature 396 (6711), 590-594 (1998)
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Pred. No. 0;
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Yaron,A., Hazubai,A., Mercurio,F., Manning,A.M., Mann,M. and Ben-Neriah,Y.
Submitte Submission
Submitted (19-OCT-1998) Immunology, Hebrew Univers
Ein Karen, Jerusalem 91120, Israel
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/db_xref="taxon:10090"
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LWDIBCGACLRVLEGEHEBLYRCIRFDMKRIVGSAXDGKIKWDLQAALDPRAFASTLC
LRTLVEHSGRVFRLQFDEPQIISSSHDDTILIMDFLNVPPSAQNETRSPSRTYTVISR
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Direct Submission

Bibmitted (05-0CT-1999) Masaru Katoh, National Cancer Center,

Submitted (05-0CT-1999) Masaru Katoh, National Cancer Center,

Genetics Division; Tsukiji 5-chome, Chuo-ku, Tokyo 104-0045, Japan

(E-mall:mkatoh@ncc.go.jp, Tel:81-3-3542-2511(ex.4402),

Fax:81-3-3541-2685)
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                                                                                                  Koike, J., Sagara, N., Kirikoshi, H., Takagi, A., Miwa, T., Hirai, M.
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Homo sapiens BTRCP2 mRNA for F-box and WD-repeats protein
beta-TRCP2 isoform B, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (05-OCT-1999) Masaru Katoh, National Cancer Center,
Submitted Division, Tsukiji 5-chome, Chuo-ku, Tokyo 104-0045, Japan
(E-mail:mkatohancc.go.jp, Tel:81-3-3542-2511(ex.4402),
Fax:81-3-3541-2685)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Biochem. Biophys. Res. Commun. 269 (1), 103-109 (2000)
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/tissue type="fetal lung"
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Goome Res. 10 (10), 1617-1630 (2000)
BX398796 BX398796
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Mus musculus adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430504E23 product:beta-transducin repeat
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HXC32221 I GI:26082733
HXC; CAP trapper.
Mus musculus (house mouse)
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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High-efficiency full.length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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/tissue_type="olfactory brain"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1. 2897
/note="beta-transducin repeat containing protein
(WAD|WGI:1338671, GB|NM_009771, evidence: BLASIN, 100%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 GAGACAGTATGTCTAACAAGCACTGCTATGAAGACTGAAAATTGTGTGGGCCAAAGGCCAAA 398
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/db_xref="taxon:10090"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Please visit our web site for further details.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-1-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,

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	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Genomic Sciences Center and Genome Exploration Research Division of Experimental Animal Research in Riken contribut prepare mouse Lissues.  Please visit our web site for further details.  Please visit our web site for further details.  URL:http://genome.gsc.riken.go.jp/.  URL:http://fantom.gsc.riken.go.jp/.  Localion/Qualifiers  1. 4502  / organism="Mus musculus" / mol_Lype="manNa" / mol_Lype="manNa" / strain="CSTBL/6J" / db_xref="PRANTOM DB:D330027D11" / db_xref="PRANTOM DB:D330027D11" / db_xref="PRANTOM DB:D330027D11" / clone="1D330027D11" / clone="1D330027D11" / clone="1D330027D11" / dev sfage="13 days embryo" / dev sfage="13 days embryo" / mol_wooling= lib="RIKEN full-length enriched mouse cDNA dev sfage="13 days embryo" / mol_wooling= lib="RIKEN full-length enriched mouse cDNA dev sfage="13 days embryo" / mol_wooling= lib="RIKEN full-length enriched mouse cDNA dev sfage="13 days embryo" / mol_wooling= lib="RIKEN full-length enriched mouse cDNA dev sfage="13" days embryo" / mol_wooling= lib="RIKEN full-length" /	tch  1284 a 998 c 1126 g 1094 t  1284 a 998 c 1126 g 1094 t  1355, Conservative 0, Mismatches 152, Indels 0, Gaps  1355, Conservative 0, Mismatches 152, Indels 0, Gaps  1357, Conservative 0, Mismatches 152, Indels 0, Gaps  1360 TICAGAATTCCTCAGAGAGAGACTGTAATAATGGCGAACCCCTAGGAAGATAATA  1372 CCAGAGAAGAATTCACTTAGAGAGATACACAGCTGTGCCAGAACCTAAGAGAATAATA  1361	CTTGCCAATGGCACTTCCAGCATGATTGTGCCCAAGCAGCAGAACTCTCAGCAAGGTAT 51  GAAAAGGAAAAGGAACTGTGTGCAAATACTTTGAGCAGTGGAGATCAGCAGTCAAGTG 41  GAATTGTGGAAACTGTTATATCCCAAATGTGTCATTACCAGTCAGAGTCAATCAA	S92 GTGTGCAAGAANTGGTACCGAGTGACGATGATGCATGCTGTGGAAGAGCTTATCGAGG

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IVSRKERSEGNYQKESDLCIKYFDQMSESDQVEFVEBLISBNCHYGGGHINSYLKPDL

QRDFTTALFEQGLDHIABNILSYLDARSLCAAELVCKEWQRVISEGNLWKKLIERWYR
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F-BOX AND WD-REPEATS PROTEIN BETA-TRCP2) homolog [Homo
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Itsues were provided by Dr. John Todd (Dept. of Medical Genetics Itsues were provided by Dr. John Todd (Dept. of Medical Genetics Mellcome Trust (MRC building Addenbrookes Hospital Cambridge) whose Trust/MRC building Addenbrookes Hospital Cambridge) whose Passistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
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                                                                                                                                                      Yokohama
                                                                                                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome Experienced in Following in Riken Genomic Sciences Center and Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to
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                                         Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN). Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC) RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-resegsc:riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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Pred. No. 4.3e-233;
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Best Local Similarity 74.58
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Nature 420, 563-573 (2002)
6 (bases 1 to 3824)
                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Meth. Enzymol. 303, 19-44 (1999)
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	RESULT 5  BX398796  LOCUS  BX398796  LOCUS  DEFINITION  BX398796  Home sapiens PLACENTA COT 25-NORMALIZED Home sapiens CDNA  CLOCKSION  BX398796  ACCESSION  BX398796  VERSION  BX398796  IG130629574  KEYWORDS  Home sapiens  CONGANISM  Home sapiens  CONGANISM  Mammalia; Butheria; Primates; Catarrhini; Hominidae; Home.  ACTESTENCE  ACTESTON  BX398796  Li, W.B., Gruber; C., Jessee, J. and Polayes, D.  TITLE  Home published  CONGANISM  CONDUCTION  DUDDDISHED  CONGANISM  CONDUCTION  COND	Genoso Genoso BP 191 Email: Librar Invitx more: http://htt	/CISSUE LYPE="FILTENING ADDIENTALIZED" //CIONE TID="Homo sapients PlacENTA COT 25-NORMALIZED" //CIONE TEAT STRAND CDNA was primed with a NotI-oligo(dT) primer: Five prime end entriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecor v sites of the pCNNSPORT 6 vector. Library was normalized."    Dest Court
478 AAACCTATGTTGCAGAGACTTTCATAACTGCTCTGCCAGCTCGGGGATTGCATCATATC 537  463 AAGCCCATGTTGCAGCGGCACTTTATCACTGCTCTTGCCAGCTCGGGGATTGGATCACTTA 522  538 GCTGAGAACATTCTGCATACCTGGATGCCTATGTGCTGCTGCAGACTTGTGTGC 597  523 GCGAAAACATTCTCCTCATACCTGGATGCCAATCCCTATGTGCTGCAGAACATTGTGTGC 597  524 GCGAAAACATTCTCCTCATACCTGGATGCCAGATCTTGTGCTGCAGAGCTTATCGGTGTGT 582  525 GCGAAAAACAGAGGATGACTGGATGCCAGATCTGTGCTGCAGAGAGTTATCGAGAGATG 657  526 AAGGAATGGTACCTGTGGAGGATGCTTTTGGAAGAGCTTATCGAGAGATG 657  527 GCGCACGGCGGTGATCTCGGAGGGATGCTTTGGAAGAGAGTGTTATTAAAAAAACAGATCTTTGGAAAAAAAA	778 CCTAAAATTATACAAGACATTGAGAATCTAATTGGAGATGTGGAAGACATAGT 837  757 CCAAAGATTATCCAGGACATTGAGAATCCAACTGGAGGTGTGGGAAGACAACA 816  838 TTACAGAGAATTCACTGCCGAAGTGAAACAACAACTGGTTTACTGTTTACAGTATGAT 897  817 TTGCAGAGAATTCACTGCCGCTCTGAAAATGTAAGGGTGTTACTGTTTACAGTATGAT 897  817 TTGCAGAGAATCCAGTGCCGCTCTGAAAAAAGAGGTGTTACTGTTTACAGTATGAT 876  898 GATCAGAAAATATCAGTGCCGCTTCGAGAAAACAGGTCTACTGTTTGCAATATGAT 876  877 GATGACAAAATTATCAGTGGCCTTCGAGACAACTATCAAGATCTGGGATAAAAGAG 936  958 TTGGAAATGCAAAATTATCAGTGGCCTCCAGGAACTACAGGTCTCACTCTCTCT		1318 ACAAGTACTIGGAATTIGTAAAGGACCTTAAATGGACCACAAAGGACATTGCCTGTTTG 1377  1297 ACGAGCACTGTGAATTIGTAAAGGACCTTAAATGGACCAAACGAGCATTGCCTGTTTG 1377  1297 ACGAGCACTGTGAGTTTGCCGCACTCTGAATGGCAAAGGCATTGCCTGTTTG 1376  1378 CAGTACCAGCACCAGCTGGTTAGTGGATCACTCTGAAATACAACATTATGGACCTTTTTTGGAC 1437  1379 CAGTACCAGCACCAGCTTGTTTAGTGGATCATCAACATTATGGTCCGTTTTTTTT

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="lason:9608"
/tissue_type="retinoblastoma"
/lab host="DH10B (phage-resistant)"
/clone=lib="NNH MGC 67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Frimer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
1 = 156 c 175 g 185 t
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UI-M-FY0-cdq-k-22-0-UI.rl NIH_BMAP_FY0 Mus musculus cDNA clone
UI-M-F80-cdq-k-22-0-UI.rl NIH_BMAP_FY0 Mus musculus cDNA clone
UAGB: 6833135 5', mRNA sequence.
CB244526
CB244526.1 GI:28366170
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                                                                                                                                                                                                                                                                             Score 650.6; DB 10; Length 709;
Pred. No. 4.9e-170;
0; Mismatches 9; Indels 4;
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sl Similarity 98.2%;
700; Conservative (
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BE782628
                                                                                                                                                                                                            CAGTAGTTCACATGATGACACAATCCTCATCTGGGACTTCCTAAATGATCCAGCTGCCCA 1727
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GCGTTGTATTCGATTTGATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAA 315
                                                                                316 AGTGTGGGATCTTGTGGCTGCTTTGGACCCCCGTGCTCCTGCAGGGACACTCTGTCTACG 375
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CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
Plate: LLAM9617 row: f column: 13
High quality sequence stop: 655.
1.709
                                            1548 AGTGTGGGATCTTGTGGCTGCTTTGGACCCCCGTGCTCCTGCAGGGACACTCTGTACG
                                                                                                                                                                                                                                         CAGTAGTTCACATGATGATGATCCTCATCTGGGACTTCCTAAATGATCCAGCTGCCCA
                                                                                                                                                  ACACTGACCTCATACTTGCCCAGGACCCATTAAAGTTGCGGTATTTAACGTATCTGCCAA
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Homo sapiens
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TITLE
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TCTGGGATAAAAACACATTGGAATGCAAGCGAATTCTCACAGGCCATACAGGTTCAGTCC 1000
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            661 TGTGGGATATGGCTTCCCCAACTGACATCACCCTCANGAGGGTGCTGGTGGGACACCCGAG 720
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Mutinae; Mushand http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
                                                                         rerererecaginacancageses and rearcacactectes and reserved 
                                                                                                                                                                                                                 ctgctgtcaatgttgtagactttgatgacaagtacattgtttctgcatctggggat 1296
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UI-M-EXO-bxj-1-06-0-UI.rl NIH_BMAP_EXO Mus musculus cDNA clone
IMAGE:5709077 5', mRNA sequence.
                                                                                                                                                                          881 ACTGTTTACAGTATGATGATCAGAAAATAGTAAGCGGCCTTCGAGACACACAATCAAGA
                               GATGTGGAAGACATAGTTTACAGAGAATTCACTGCCGAAGTGAAACAAGCAAAGGAGTTT
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/clone="IMAGE:5709077"
/tissue type="whole brain"
/dev_stage="embryo 15.5 dpc"
/lab_host="embryo 15.5 dpc"
/lab_host="DH108 (TI phage resistant)"
/clone_lib="NIH_BMAP_EX0"
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/strain="C57BL/6"
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/dev stage="mmbryo 13.5,14.5,16.5,17.5dpc"
/lab_hose="DH10B (TI phage resistant)"
/lab_hose="DH10B (TI phage resistant)"
/lab_hose="DH10B (TI phage resistant)"
/lone lib="MIH BYAP FYO."
/lone Research, 6:791-806,
/lone Remaining and Soarces, Genome Research, 6:791-806,
/lone First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with DEOR I adaptor, digested with NorI and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGAGG. This library was created for the University lowe Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement. Dr. Jim Lin, University of lowa
CDNA Library preparation: Dr. M. Bento Soares, University of lowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of lowa
DNA Sequencing by: Dr. M. Bento Soares, University of lowa
DNA Sequencing by: Dr. M. Bento Soares, University of lowa
Clone Distribution: MGC clone distribution information can be
ftup://image.lln.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
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   Mus musculus
Mus musculus
Mus musculus
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 776)
Nath-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE: 6833135"
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                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini; Hominidae, Homo.
1 (Sases 1 to 652)
Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09
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6, 14059
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKEZ); Email s.wiemann@dKz- heidelberg.de),
sequenced by GBF (National Research Centre for Biotechnology Ltd
Braunschweig/Germany) within the cDNA sequencing consortium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAATTGGTGCGTTGTATTCGATTTGATAACAAGAGGATAGTCAGTGGGGCCTATGATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="414 (synonym: htes3)"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sall"
166 c 138 g 183 t
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No sl sequence available.

This clone (DRF20134HEPE) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers
                                                                               652 bp mRNA linear DKFZp434M1528_r1 434 (synonym: htes3) Homo sapiens DKFZp434M1528_s', mRNA sequence.
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Pred. No. 9.3e-166;
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/db_xref="taxon:9606"
/clone="NkE78434M1528"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH108"
                                                                                                                                                                                          AL044095.1 GI:5432322
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/note="Organ: brain; Vector: pXX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Benaīdo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNa was size fractionated on a 1% agazose gal. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, 11gated with EcoR I adaptor, digested with Not I, and then cloned directionally into pXX.Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCGTGAA. This library was created for the University of lowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System, supported by National Institutes of Mencal Health (NTHM), Health, Ph.D., program coordinator."
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5', mRNA sequence.
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                  359 ATCTGCCAATACCAGGATGAGCAACAACAACAATAACAATCAAACTACTGCCCAGTTTCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.

Email: Gapber:Gemail.nih.gov
Tissue Procurement. AICG
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at:
Plate: LLAM13456 row: i column: 15
ATCTGCCAATACCAGGATGAGCAACAACAGTAACAATCAAACTACTGCCCAGTTTCCCTG
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973 bp mRNA linear EST 05-FEB-2002
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(bases 1 to 973)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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CDNA Library Arrayed by: The I.M. A.G.B. Conscortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can littp://inage.llnl.gov.
Thtp://inage.llnl.gov. column: 04
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/clone_lib="NH10B (phage-resistant)"
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Library constructed by Technologies."
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'clone="IMAGE:5502075'
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mRNA linear EST 12-SEP-2002 sapiens cDNA clone IMAGE:6501709

BUS07728
AGENCOURT 10095724 NIH MGC 71 Homo

5', mRNA sequence. BUS07728

BU507728.1 GI:22813961 EST. Homo sapiens (human) sapiens (human)

ACCESSION VERSION KEYWORDS SOURCE

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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bukaryota, Metheria, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 887)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through Lhe I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAMI4656 row: j column: 14

High quality sequence stop: 630.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          þe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Pred. No. 4.7e-162;
0; Mismatches B;
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CAAAGATCGTTCCATTGCTGTATGGGATATGGCCTCCCCAACTGACATTACCCTCCGGAG 1220
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                                61 GGACGCCAAGTCACTGTGTGCTGCTGAGGTGCAAGGAATGGTACCGCGTGACGTC 120
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     661 CAAAGACCGTTCCATCGCTGTGTGGGATATGGCTTCCCCAACTGACATCACCTCCCCTAACGAG
                                                                                                                                      241 GAACGCTCCTCCACCATCCTTTTATAGAGCGCTTTATCCTAAAATCATACAAGACATTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 GACAATAGAGTCCAATTGGAGATGTGGGGGGCGACATAGTTTACAGAGAATCCACTGCGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 CTCAGACTCCACCGTCAGAGTGTGGGATGTAAATGCAGGTGAGATGCTAAACACATTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCACCATTGTGAAGCAGTTCTGCACTTGCGTTTCAATAATGGCATGATGGTGACCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601 TCACCACTGTGTAGCCGTTCTGCACCTGCGCTTCAATAATGGCATGATGGTGACCTGTTC
561 GGATGCCAAATCACTATGTGCTGCTGAACTTGTGTGCAAGGAATGGTACCGAGTGACCTC
                                                                                                       TGATGGCATGCTGTGGAAGAAGCTTATCGAGAGAATGGTCAGGACAGATTCTCTGTGGAG
                                                                                                                                                                                                                                                         181 AGGCCTGGCAGAGGCAGAGGCTGGGGACAGTACTTATTCAAAAACAACCTCCTGATGA
                                                                                                                                                                                                                                                                                                               GAAIGCICCICCCCAACICITITIATAGAGCACTITAICCIAAAAITAIACAAGACAITGA
                                                                                                                                                                                                                                                                                                                                                                                                               801 GACAATAGAATCTAATTGGAGATGTGGAAGACATAGTTTACAGAGAATTCACTGCCGAAG
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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Tissue Procurement: ATCC
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/clone="IMAGE: 6841315"
/tissue_type=="Whole brain"
/dev stage="Whole brain"
/dev stage=="Whole brain"
/dev stage=="Image resistant"
/lab_host="DH10B (TI phage resistant)"
/clone_lib="WhitH_RNAP_QH0"
/note="Organ: Brain; Vector: pyx- Asc; Site_1: EcoR I;
/clone] brain; Vector: pyx- Asc; Site_1: EcoR I;
/note="Organ: Brain; Vector: pyx- Asc; Site_1: EcoR I;
/site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pyx-Asc vector. The library tag;
sequence located between the Not I site and the polyh tail
is CGAACTGAAT. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Bervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                              CB520936 744 bp mRNA linear EST 28-MAR-2003 UI-M-GHO-cel-p-18-0-UI.rl NIH_BMAP_GHO Mus musculus cDNA clone IMAGE: 6841315 5', mRNA sequence.
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CTCCCCTCCTCTCCTTTCACCTCTGCACCTAGTTTTTCCCATTGGTTCCAGACAAA 2108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs.remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefil.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                   542 CTCCCCTCCTCTCTCTCTTCACCTCTGCACCTAGTTTTTTCCCATTGGTTCCAGACAA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 744)
NIH-WGC http://mgc.nci.nih.gov/.
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                                                                                                  GGTGACTTATAAATATTTAGTGTTTTGCCAGAA 2143
                                                                                                                                   GGTGACTTATAAATATATTTAGTGTTTTTGCCAGAA 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   program coordinator,
184 c 202 g
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Location/Qualifiers
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/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                        CB520936.1 GI:29354291
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AUTHORS
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1100

1040

300

860

360

920 420 086 480

800

1160

900

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/organisma."Homo sapiens"

/mol type="mRNA"

/db xref="taxon:9506"

/db xref="taxon:9506"

/clone="INAGE:354499"

/tissue_type="Burkitt lymphoma"

/lab host="DH10B (phage-resistant)"

/clone=lib="NIH MGC_B"

/note="Transparant lymph" Westor: poTBT; Site 1: XhoI; Site 2:

ECORI; CDNA made by Oligo-dT priming. Directionally

cloned into ECORI/XhoI sites using the following 5'

adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis Xit

(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                              BE269297 691186356F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3544549 5',
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 692)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.

Email: Gapbs-rewaril.nih.gov

Email: Gapbs-rewaril.nih.gov

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incytte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCN239 row: o column: 14

High quality sequence stop: 610.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 2.3e-158;
0; Mismatches 12;
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ilarity 97.7%;
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// Organism="MENRA"

// Darie="Laxon:9606"

/ Clone="InAGE:3530341"

/ Lissue type="Inbadomyosarcoma"

/ Lissue type="Inbadomyosarcoma"

/ Lissue type="Inbadomyosarcoma"

/ Lib host="DHIOR (phage-resistant)"

/ Clone="Organismusof=">
/ Vector: porBR: Site 1: EcoRI;

/ Noce="Organismusof=">
/ Nota made by oligo-dT prining: Site 2: XhoI; cDNA made by oligo-dT prining: Site 2: XhoI; cDNA made by oligo-dT prining: Site 2: Adaptor: GGCAGGG(6). Size-selected -550bp

for average insert size 1: Bkb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit

/ Stratagene, and Superscript II RT (Life Technologies)."
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Drosophila melanog Human beta TrCP (b Differentiation In Beta-TRCP.N/SKP2.C CDNA encoding huma Human prostate exp Drosophila melanog Human breast cell Human foetat liver Probe #2778 for ge Human brain expres

AAK52260 AAI59364 ABL06083 AAZ09025 AAX09025 ABK43155 ABK43155 ABK46075 ABA60895 ABA60895 ABA60895 ABA648075 ABA648075 ABA648075 ABA648075 ABA648075 ABA648075

breast cell foetal liver #12638 for g brain expres

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ALIGNMENTS

bone marrow #2761 for ge #2870 used t #2737 used t

AAK28263 AAI12828 AAI34184 AAI02746 ABS27866

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Beta-transducin repeat containing protein; beta-TrcP; Skplp; proteosome degradation pathway; Mu protein; beta-catenin; protecome degradation pathway; HVV-1; cellular protein; langual immune deficiency virus; HVV-1; cellular protein; thosphorylated brotein; tumour; apoptosis; Alzheimer's; antivizal; antitumour; cell cycle regulation; protein degradation; and antivizal; antimmour; cell cycle regulation; protein degradation; tumour necrosis factor; ss.
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/product= beta-TrcP
/note= "beta-transducin repeat containing protein"
                                                                                                                                                                                                                 cDNA encoding a human beta-transducin repeat containing protein
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AAX86501 standard; cDNA; 2151 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a human beta-transducin repeat containing protein (beta-TrcP). The protein directs proteins to the proteosome degradation pathways. The protein is able to interact with the Vpu protein of human immune deficiency virus-1 (HIV-1), callular proteins impune of the protein of protein of human immune deficiency virus-1 (HIV-1), callular proteins in the protein of the protein of proteins and thus their targeting to proteosomes for degradation. Depending on whether the protein controls inhibited or promoted, the result may be delayed breakdown of CD4 (in cases of HIV-1 infection); increased activity of IMB (and thus reduced activity of NFkappaB) and increased degradation of mutant bC in tumour calls, or increased bc survival (and reduced apoptosis) in Alzheimer's patients. The beta-TrCP protein, and its active peptide fragments, or its nucleic acid, are used to screen for anti HIV-1 agents (antivirals), antitumour agents that disrupt call cycle regulation or protein are also useful for treating osteo-articular inflammation or acute inflammation associated with release of tumour necrosis factor.

(Updated on 20-MAR-2003 to correct PA field.)
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This DNA encodes human beta-TrCP, an F-box/WD protein family member, which has been shown to have homology to human E3 ubiquitin ligase (E3). E3 enhances ubiquitination of phosphorylated I-kappa-B, an inhibitor protein of nuclear factor kappa-B (WF-kappa-B). Understanding I-kappa-B degradation via the ubiquitin pathway is useful for identifying addition via the ubiquitin pathway is useful for identifying activation of NF-kappa-B. In vitro analysis suggests that deletion of this process for use in treating diseases associated with activation of NF-kappa-B. In vitro analysis suggests that deletion of he F-box results in a protein that functions as a dominant negative molecule in vivo. Translant over-expression of delta-ber_TrCP (a deletion mutant) inhibited the degradation of endogenous I-kappa-B-alpha in stimulated Jurkat cells, resulting in accumulation of phosphorylated I-kappa-B-alpha-B. and beta-TrCP can be used to modulate NF-kappa-B to treat inflammatory diseases, autoimmune diseases, cancer and viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 GGCACTTCCAGTATGATTGTGCCCAAGGAAACTCTCAGCAAGCTATGAAAAGGAA 360
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                                                                                                                          Hatzubai
                                                                                                                                                                                                                                                                                          Polypeptide enhancing phosphorylated lkappaB ubiquitination useful treating disorder associated with NF-kappaB activation e.g. cancer, comprising amino acid sequence of human E3 ubiquitin ligase or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21; Length 2151;
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                                                                                                                       Davis M,
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                                                                                                                    Ben-eriah Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 72; 77pp; English.
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                              (SIGN-) SIGNAL PHARM INC.
(YISS ) YISSUM RES & DEV CO.
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Matches 2151; Conservative
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                                                                                                                                                   Yaron A;
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Lavon I,
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                                 TTTGATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAATTAAAGTGTGGGATCTT
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TTTGATAACAAGAGGATAGTCAGTGGGGCCTATGATGGAAAATTAAAGTGTGGGGATCTT
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Novel nucleic acid for screening compounds useful for treating proliferative and differentiative disorders such as cancer and immune disorders comprises sequences encoding ubiquitin ligases -Nucleic acids encoding substrate-targeting subunits of ubiquitin ligases with F-box motifs (F-box proteins) are useful for diagnosis of proliferative and differentiated related disorders by measuring FBP gene expression. Cells expressing such proteins or their fragments are useful for screening compounds. The compounds are agonists or anteagonists, which are useful for treating a proliferative or differentiative disorder in a mammal such as breast, ovarian and prosetate cancer and small also major opportunistic infections, immune disorders, cardiovascular diseases and inflammatory disorders. FPP protein, are also useful in diagnosis of the disorders. Disclosure, Figure 3b, 3c, 3d; 245pp; English

Sequence 2151 BP; 628 A; 467 C; 513 G; 543 T; 0 other;

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ligases) which can be used for the targetted degradation of a target polypeptide in vivo. Targetted degradation is achieved by expressing the target to the unlearaction domain of the target polypeptide and thereby recruiting the target polypeptide on thereby recruiting the target polypeptide increasing the level of a target polypeptide and for creating or increasing the level of a target polypeptide and for creating and expressing a destabilized polypeptide which is subjected to SCF mediated proteolysis. Degrading any desired protein in a cell is weful for preventing or treating diseases caused by the presence of abnormal amount of the specific polypeptides, for drug discovery and for gene therapy. Diseases treated include cancer, by degradation of concoproteains, Huntington's disease, other proliferative disorders and microbial infections. The method provides a quick and easy alternative to gene knockout technology. The target polypeptide can be degraded at all stages, or a specific stage, of development in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ubiquitin ligase, SCF, F-box protein, targeted degradation, destabilisation; proteolysis; drug discovery; gene therapy; cancer; oncoprotein, Huntington's disease; gene knockout; delivery systems;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modulating polypeptide levels in a cell, diagnosing and treating tumor, involves altering levels of proteins such as S-phase kinase associated proteins 1, 2 and cullin/CDC53 proteins
                                         <u>AACAACAGTAACAATCAAACTACTGCCCAGTTTCCCTGGACTAGCCGAGGAGCAGGGCTT</u>
                                                                  AACAACAGTAACAATCAAACTACTGCCCAGTTTCCCTGGACTAGCCGAGGAGGAGGCTT
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                                                                                                                                                                                                    Cytostatic; immunomodulator; cardiant; antiinflammatory; antimicrobial; proliferative; differentiative disorder; Skp2; F-box protein; cancer; ubiquitin ligase; breast cancer; prostate cancer; ovarian cancer; small cell lung carcinoma; immune disorder; parathyroid adenoma; FBP; inflammatory disorder; lymphoma; major opportunistic infection; certain cardiovascular disease; human; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCGGCGATTATGGACCCGGCCGAGGCGGTGCTGCAAGAAGGCACTCAAGTTTATGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Screening compounds for treating proliferative disorders, e.g. breast cancer or prostrate cancer, infections or immune disorders, comprises detecting a change in the activity of Skp2 with either p27 or Cks1
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                                                                                                                                                               of Human F-box protein FBP1 SEQ ID No 1.
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The invention relates to a complex of protein-protein interactions (forming a protein-protein interaction map, PIM) in adipocyte cells as defined in the specification, or polymucleotides in adipocyte cells as defined in the specification, or polymucleotides in adipocyte cells and a method of selecting a modulating compound in adipocyte cells, by cultivating a recombinant host cell on a selective interacting polypeptides and a method of selecting a modulating compound and a reporter gene the medium containing a modulating compound and a reporter gene the medium containing a modulating compound and a reporter gene the medium containing a first hybrid polypeptide and DNA binding compound which two vectors, where the first vector comprises a polymucleotide encoding a first hybrid polypeptide and DNA binding domain and the second vector comprising a polymucleotide encoding a second hybrid polypeptide and an activating domain that activates the toxic reporter gene, when the first and second hybrid polypeptides interact and selecting the modulating compound which inhibits the crowth of the recombinant host cell (i.e. using the yeast two-hybrid system). The complexes are useful for identifying compounds that modulate the protein-protein interactions and useful for treating obesity and metabolic diseases. The interactions between the proteins of the complex further define a set of selected interacting domains, SID. The present sequence encodes a member of the protein complex of the protein in the yeast two-hybrid assay.

Note: The present sequence was not displayed in the specification but
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1261 TITGAIGACAAGTACATIGITICIGCAICIGGGGAIAGAACTATAAAGGIAIGGAACACA 1320
                                                         GAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTCGA
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Novel complex of protein-protein interactions in adipocyte cells for identifying compounds that modulate the protein-protein interactions and useful for treating obesity and metabolic disorders

Claim 2; Page -; 125pp; English.

Jockers

28-DEC-2001; 2001WO-EP15423 02-JAN-2001; 2001US-259377P (HYBR-) HYBRIGENICS. (CNRS ) CENT NAT RECH SCI Legrain P, Marullo S, WPI; 2002-583612/62. P-PSDB; ABG69473

WO200253726-A2 Homo sapiens

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non-insulin diabetes mellitus, obesity, selected interacting domain,
SID; protein-protein interaction map, PIM, anorectic, metabolic disorder.
                                                                                                                                                                                                                                                                                                                                                          Human cDNA encoding bait protein beta-TrCP1.
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ABS51009,

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Note: The present sequence was not displayed in the specification but was obtained from its Genbank entry by the indexer.

Sequence 2151 BP; 628 A; 467 C; 513 G; 543 T; 0 other;

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	1441 GAATGTGGATGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTCGA 1500 	1501 TITGATAACAAGAGATAGTCAGTQGGCCTATGATGGAAAATTAAAGTGTGGGATCTT 1560 		1621 CATTCCGGAAGAGTTTTGGACTACAGTTTGAAGTTCCAGATTGTCAGTGTTCACAT 1680 		1741 CGTICCCCTTCTCGAACATACACCTACATCTCCGGATAAATAACCATACACTGACCTCAT 1800 	1801 ACTTGCCCAGGACCCATTAAAGTTGCGGTATTTAACGTATCTGCCAATACCAGGATGAGC 1860 	1861 AACAACAGTAACAARCTACTGCCCAGTTTCCCTGGACTAGCCGAGGAGGAGGCTT 1920 	1921 TGAGACTCCTGTTGGGACACAGTTGGTCTGCAGTCCAGGACGGTCTACTCAGCACA 1980		TITIAAACCICCCCCCCCCCCCCCCCCCCCCCCCCCCCC	2101 CAGACAAAGGTGACTTATAAATATATTTAGTGTTTTGCCAGAAAAAAAA	ILT 8 30079 AAH90079 standard; cDNA; 3220 BP.	ААН90079; 01-ОСТ-2001 (first entry)	Human bone marrow cDNA, SEQ ID NO: 323.	numari pour mation; antilitammatory; cytogrants; inturpirective; antivizal; antibacterial; antilingal; anti-HIV; haemostatic; immunosuppressive; gene therapy; cytokine cell proliferation; cancer; cell differentiation modulator; immune disorder; infection; cancer; human immunodeficiency virus; HIV; autoimmune disorder; haemophilia; ss. Homo sapiens.
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Pred. No. 0;
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ing J, Werhman T, Xi
Zhou P, Drmanac RT;
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2000US-052317.
2000US-0528042.
2000US-06280312.
2000US-0653450.
2000US-0662191.
2000US-0663036.
2000US-0663036.
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Best Local Similarity 99.6%;
Matches 2136; Conservative
                                                                                 2000WO-US34960
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            WO200153453-A2
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09-JUL-2000;
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03-AUG-2000;
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The present sequence is a cDNA obtained from Incyte clone 3239149 of COLAUCTO1 library. It encodes cell signalling protein-12 (CSIGP-12). It is expressed in musculo-skeletal, gastrointesinal and nervous tissues. Fragments of CSIGP encoding nucleic acid can be used as hybridisation probe for detecting CSIGP related sequences or allelic hybridisation probe for detecting CSIGP related sequences or allelic than variants. Recombinant CSIGP can be produced in host cells by transforming them with genetically engineered vectors. Agonists or antagonists can be used in the treatment of cell proliferative and inflammatory disorders associated with decreased or increased CSIGP expression. CSIGP is used in the diagnosis, prevention and treatment of cell proliferative disorders like attentosclerosis, cirrhosis, cancer, hepatitis and inflammatory disorders disorders like AIDS, Addison's disease, multiple sclerosis, etc.
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Best Local Similarity 99.7°
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Yang J;
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P-PSDB; AAY44249.
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Baughn MR,
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491 AGAGAGATTCATAACTGCTCTGCCGCGCGTACGATATTGCTGGAACATTC 550  551 TGTCATACCTGGATGCCAATTCACTGTGCTGCTAACTGTGTGCAAGGAATGGTACC 610  551 TGTCATACCTGGATGCCAATTCACTTGTGCTGCTGAAGGAATGGTACC 610  611 GAGTACCTTGGAGGATGCCTGTGGAAGAAGCTTATCGAAGAATGGTACAAGTACT 670  611 GAGTCCTCTGAGGCATGCCTGTGAAGAAGCTTATCGAAGAATTGTACAAGAATT 670  611 GAGTCACTCTGAGGCATGCCTGTGAAGAAGCTTATCGAAGAATTGTACAAATTATCAAAACAAAC	1091 ACACGTTGATTCACCATTGTGAAGCAGTTCTGCACTTCAATAATGGCATGATGG   1150

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                                              TATTITATICAAAACAAACCICCIGACGGGAAIGCICCICCCAACICITITITATAGAGCA
                                                                                                                                                                   CATAGITITACAGAGAATICACIGCCGAAGIGAAACAAGCAAAGGAGITITACIGITITACAG
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                                                                                       CTTTATCCTAAAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGAAGA
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                                                                                                                                                                                                                                         The present sequence is one of 251 novel human polynucleotides expressed in the bone marrow. The polynucleotide and the polypeptide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation. System disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polynucleotide or the protein it condes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of chemical compounds as potential drugs.
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                                                                                                                                            Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders -
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Zhang J;
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    C, Asundi V, Chen
Xue AJ, Yang Y, Z
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Boyle BJ, Tang YI,
Wang J, Werhman T, X
Zhou P, Drmanac RT;
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production of other cytokines in other cell populations. The polymorleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, insulin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.

Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                            Sequence 3003 BP; 807 A; 703 C; 721 G; 772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
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  AGCAGGGCTTTGAGACTCCTGTTGGGACACAGTTGGTCTGCAGTCGGCCCAGGACGGTCT
                                                                                                                                                                                                                                   ACTCAGCACAACTGATTCAGTGCTGCTATCAGAAGATGTCTTCTATCAATTGTGAA
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                                                                   CAGGATGAGCAACACAGTAACAATCAAACTACTGCCCAGTTTCCCTGGACTAGCCGAGG
                                                                                                                                                                                AGCAGGCTTTGAGACTCCTGTTGGGACACAGTTGGTCTGCAGTCGGCCCAGTACGGTCT
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R, Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                        2241 CCATTGGTTCCAGACAAAGGTGACTTATAAATATATTTAGTGTTTTTGCCAGAA
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2000US-0560875.
2000US-053025.
2000US-065335.
2000US-0654336.
2000US-063351.
2000US-0633351.
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Zhao QA,
Xue AJ, 1
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                                                                                                                                                                                                                                                                                                                                                               Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor; haematopoiesis, tissue growth factor; mmunomodulatory; cancer; leukaemia; nervous system disorder; arthritis, inflammation; ss.
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Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
TGATTGGAACTTTTAAACCTCCCCTCCTCTCCTTTCACCTCTGCACCTAGTTTTTTC
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                                                                         CCATTGGTTCCAGACAAAGGTGACTTATAAATATTTAGTGTTTTTGCCAGAA 2143
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Wang ZW;
                                                                                                CCATTGGTTCCAGACAAAGGTGACTTATAAAATATATTAGTGTTTTGCCAGAA
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Wang D, Wang J, Zhang J, Ren F, Chen R,
Yang Y, Wejhrman T, Goodrich R;
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Zhao QA,
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                                                                         Human, cytokine, cell proliferation, cell differentiation, gene thy vaccine, peptide therapy, stem cell growth factor, haematopoiesis, tissue growth factor, immunomodulatory, cancer, leukaemia, nervous system disorder, arthritis, inflammation, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C, Drmanac RT, Asundi V, Zhou P,
Wang D, Wang J, Zhang J, Ren F, Chen
Yang Y, Wejhrman T, Goodrich R;
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Pred. No. 0;
0; Mismatches
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                                       NO 2230
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Best Local Similarity 99.6%;
Matches 2024; Conservative (
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01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-06549361.
20-OCT-2000; 2000US-0633551.
30-NOV-2000; 2000US-0728422.
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27-APR-2000; 2000US-0560875.
20-JUN-2000; 2000US-0598075.
                                     Human polynucleotide SEQ ID
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P-PSDB; AAM79568
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06-NOV-2001
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Zhao QA,
Xue AJ,
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TGTATTCGATTTGATAACAAGAGGATAGTCAGTGGGGCCTATGATGAAAATTAAGTC
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The present invention describes an F-box motif protein of ubiquitin ligase SCF complex which promotes the ubiquitination of IkappaB or beta-catenin and is constituted by Skpl protein, Cull protein and a complex (SCF complex) of F-box protein containing F-box motif and WD40 complex (SCF complex) of F-box protein containing F-box motif and WD40 or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin ligase FWD1 protein) and (AAB12813, which is human beta-transducin ligase FWD1 protein (beta-TrCP). The F-box protein can be used for the gene therapy of colon cancer by being recombined to a virus vector. The present sequence encodes the human beta-TrCP protein from the

Sequence 1707 BP; 514 A; 349 C; 414 G; 430 T; 0 other;

present invention.

ubiquitin ligase SCF complex which promotes the I kappaB or beta-catenin

Disclosure, Fig 17; 19pp; Japanese.

(KAGA-) KAGAKU GIJUTSU SHINKO

WPI; 2000-485550/43. P-PSDB; AAB12813.

F-box protein of ubiquitination of

98JP-0343437 98JP-0343437

02-DEC-1998; 02-DEC-1998;

us-09-601-168b-1.rng

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Ubiquitin ligase SCF complex; F-box protein; ubiquitination; IkappaB; beta-catenin; Skpl; Cull; F-box mctif; WD40 repeat mctif; FWD1; gene therapy; colon cancer; beta-transducin repeat containing protein; beta-TrCP; ss.
                                                                         Human beta-transducin repeat containing protein (beta-TrCP) cDNA
AAA73132 standard; cDNA; 1707
                                                   (first entry)
                                                 27-NOV-2000
                         AAA73132,
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Homo sapiens.

0 249 309 240 369 300 549 609 189 120 429 TGTGTCAAATACTTTGAGCAGTGGTCAGATCAGATCAAGTGGAATTTGTGGAACATCTT 360 489 420 480 699 600 09 70 ATGGACCCGGCCGAGGCGGTGCTGCAAGAGGCACTCCAAGTTTATGAATTCCTCAGAG ATGGACCCGGCCGAGGCGGTGCTGCAAAGGCACTCAAGTTTATGAATTCCTCAGAG AGAGAAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATACCAGAGAATTCACTT AGCACTGCTATGAAGACTGAGAATTGTGTGGCCAAAACAAAACTTGCCAATGGCACTTCC AGCACTGCTATGAAGACTGAGAATTGTGGCCCAAAACAAAACTTGCCAATGGCACTTCC AGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTATGAAAAGGAAAAGGAACTG AGTATGATTGTGCCCAAGCAACGGAACTCTCAGCAAGCTATGAAAAGGAAAAGGAACTG TGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGAATCAAGTGGAATTTGTGGAACATCTT ATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCGTATCTTAAAACCTATGTTG ATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCGTATCTTAAACCTATGTTG CAGAGAGATTTCATAACTGCTCTGCCAGCTCGGGGATTGGATCATATCGCTGAGAACATT CAGAGAGATTTCATAACTGCTCTGCCAGCTCGGGGATTGGATCATATCGCTGAGAACATT CGAGTGACCTCTGATGGCATGCTGGAAGAAGCTTATCGAGAAATGGTCAGGACAGAT CGAGTGACCTCTGATGGCATGCTGTGGAAGAAGCTTATCGAGAGAATGGTCAGGACAGAT AGAGAAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATACCAGAGAATTCACTT .; 21; Length Indels 0 DB Ouery Match
79.4%; Score 1707; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 130 61 121 250 181 310 241 301 430 361 421 610 190 370 490 550 481 g d ò g  $\delta$  $\dot{\delta}$ Db  $\delta$ Ωp ò g à 셤 g ò  $\delta$ 8 d

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAW78329-AAM89302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITIATGAATTCCTCAGAGAGAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATA
                                                                                                                                                                                                                                                            Human, cytokine, cell proliferation; cell differentiation; gene thy
vaccine; peptide therapy; stem cell growth factor; haemacopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation; ss.
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Wang D, Wang J, Zhang J, Ren F, Chen R, Wa
Yang Y, Wejhrman T, Goodrich R;
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llarity 99.0%; Pred. No. 0;
Conservative 0; Mismatches
  TCTCGAACATACACCTACATCTCCAGA 1707
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                                                                                                                                                                                                                            Human polynucleotide SEQ ID NO 260.
                                                                                                       ВР
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27-AFR-2000; 2000US-0560875.
20-UJN-2000; 2000US-0590075.
19-UJN-2000; 2000US-0620325.
01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-0653561.
20-OCT-2000; 2000US-063325.
30-NOV-2000; 2000US-0728422.
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                                                                                                                                                                                   (first entry)
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P-PSDB; AAM78582.
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Best Local Similarity
Matches 1708; Conserv
                                                                                                       AAK51715 standard;
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Zhao QA,
Xue AJ,
  1681
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Query Match Best Local Similarity

TYPE: DNA ORGANISM: Homo sapiens

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## ALIGNMENTS

Sequence 17, Application US/09832161; Publication No. US20030166587A1; GENERAL INFORMATION:

US-09-832-161-17

APPLICANT: Manning, Anthony M.
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APPLICANT: Ben-Neriah, Yinon
APPLICANT: Baris, Mati
APPLICANT: Bavis, Mati
APPLICANT: Hatrubai, Ada
APPLICANT: Hatrubai, Ada
APPLICANT: Aron, Avraham
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FILE REFERENCE: 5914-090-999  CURRENT APPLICATION NUMBER: US,10/042,417  CURRENT FILING DATE: 2002-01-07  PRIOR APPLICATION NUMBER: 60/260,179  PRIOR FILING DATE: 2001-01-5  NUMBER OF SEQ ID NOS: 89  SOFTWARE: Patentin Ver. 2.0  SEQ ID NO 1  LENGTH: 2151  TYPE: DATE  TYPE: DATE  SOFTWARE: Patentin Ver. 2.0  SEQ ID NO 1  LENGTH: 2151  TYPE: DATE  SOFTWARE: PATENTING  SOFTWARE: PATENTIN	Query Match         100.0%;         Score 2151;         DB 13;         Length 2151;           Best Local Similarity 100.0%;         Pred. No. 0;         0 <td>  1   TGGGGATTGGGCTGGGCGCGGGGGGGGGGGGGGGGGGGG</td> <td>  121   TCTCAGAGAGAGAGATTTTTTTTTTTTTTTTTTTTTTTT</td> <td>29 241 IGITIAGCAAGCACTGCTAIGAAGACTGAGAATIGIGGGCCAAAACAAACTTGCCAAT 300  </td> <td>361 AAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGCAAGTGGAATTTGTG 4  361 AAGGAACTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGTGGAATTTGTG 4  361 AAGGAACTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTGGAATTTGTG 4  421 GAACATCTTAATACCCAAATGTGTCAACATGAGGCAATAGGGCAATAAA 4</td> <td>  Db   421 GAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCGTATCTTAAA 480</td> <td>541 GAGAACATTCTGTCATACCTGGAATGCCAAATCACTATGTGTGTCTTATGTGTGTG</td> <td>661 AGGACAGATCTCTGGGAGAGGCCTGGCAGAGGAGGATGGGGACAGTATTATTC 72  661 AGGACAGATCTCTGGAGAGGCCTGGCAGAACGAAGAGGATGGGGACAGTATTATTC 72  661 AGGACAGATTCTCTGGGAAGGCCTGGCAGAACGAAGAGATGGGGACAGTATTATTC 72</td> <td>  Oy   721 AAAAAAACCTCCTGACGGAATGCTCCTCCAACTCTTTTTATAGAGCACTTTATCCT 780</td> <td>or manitathadhan tangadhaildan kalidangaldigangan</td>	1   TGGGGATTGGGCTGGGCGCGGGGGGGGGGGGGGGGGGGG	121   TCTCAGAGAGAGAGATTTTTTTTTTTTTTTTTTTTTTTT	29 241 IGITIAGCAAGCACTGCTAIGAAGACTGAGAATIGIGGGCCAAAACAAACTTGCCAAT 300	361 AAGGAACTGTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGCAAGTGGAATTTGTG 4  361 AAGGAACTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGTGGAATTTGTG 4  361 AAGGAACTGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTGGAATTTGTG 4  421 GAACATCTTAATACCCAAATGTGTCAACATGAGGCAATAGGGCAATAAA 4	Db   421 GAACATCTTATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCGTATCTTAAA 480	541 GAGAACATTCTGTCATACCTGGAATGCCAAATCACTATGTGTGTCTTATGTGTGTG	661 AGGACAGATCTCTGGGAGAGGCCTGGCAGAGGAGGATGGGGACAGTATTATTC 72  661 AGGACAGATCTCTGGAGAGGCCTGGCAGAACGAAGAGGATGGGGACAGTATTATTC 72  661 AGGACAGATTCTCTGGGAAGGCCTGGCAGAACGAAGAGATGGGGACAGTATTATTC 72	Oy   721 AAAAAAACCTCCTGACGGAATGCTCCTCCAACTCTTTTTATAGAGCACTTTATCCT 780	or manitathadhan tangadhaildan kalidangaldigangan

CAGGCACATAAACTCGTATCTTAACAGCCCGGGATTGGATCATCGCGGGATTGGATCATCGCGGGTCGGGGATCATTGGTGCATCGTATCGCATCTGTGCCAACTGTGTGCAACTGTGTGCAACTGTGTGCAACTGAACTGTGTGCAACTGAACTGTGTGCAACTGAACTGTGTGCAACTGTGTGCAACTGAAGGGTTATCGAGAAATGGTGGAAGGAA	CTCCTGGGGGGGCCTGGGAACGAACGAACGAACGAACGATTTTTTTT
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658 GICAGGACAGATICICIGIGGAGAGGCTGGCAGAACGAAGAGGATGGGGACAGTATTTA 	718 TTCAAAACAAACCTCCTGACGGGAATGCTCTCCCCAACTCTTTTTATAGGCGCTTTAT	OY 778 CCTAAATTAIACAAGACAITGAGACAATAGAATCTAATTGGAGATGTGGAGAGACATAGT 937	Oy 838 TTACAGAGAATTCACTGCCGAAGTGAAACAAGCGAAGGAGTTTACTGTTTACAGTATGAT 897	OY 898 GATCAGAAAATAGTAAGCGGCCTTCGAGACACACAATCAAGATCTGGGATAAAAACA 957	Oy 958 TIGGAAIGCAAGGAATTCTCACAGGCCATACAGGTTCAGTCTCTCTC	Oy 1018 GAGAGAGTGATCATAACAGGATTCATCGGATTCCAGGGTCAGAGTGTGGGATGAATACA 1077	Oy 1078 GGTGAAATGCTAAAGGGTTGATTGACGATTGTGAAGGGGTTCTGGGACTTGCGTTTGAAT 113	Oy 1138 AATGGCATGATGGTGACCTGCTACGAAGATCGTTCCATTGCTGTATGGGATATGGCCTCC 1197	Oy 1198 CCAACTGACATTACCTCCGGAGGGTGCTGGACGGACCGAGCTGCTGTCAATGTTGTA 125'	0y   1258 GACTTTGATGACAAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTATGGAAC 1317	Oy 1318 ACAAGTACTIGIAAATTIGIAAGACCTTAAATIGACACAAACGAGGCATTGCCTGTTG 137	Oy 1378 CAGTACAGGACAGGCTGGTAGTGAGTGAGTGACAACAACAACAATATAGGATTATGGGAC 143	Oy 1438 ATAGAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATT 149°  1313 ATTGAATGTGGTGCCTGTTTAAGAGTCCTAGAGGGAATGAAGAGTCCCGATGCATG 1313 ATTGAATGTGGTGCCTGTTTAAGAGTCCTAGAGGAATGAGAAATGTGGTGCCTGTTAAGAGTCCTAGAGGAATGAGAAGACCTGCTGTGTGAAGAGAATGAGAAGAGTGTGCATGCA	Oy 1498 CCATITGAIAACAAGAGGAIAGICAGIGGGGCCIAIGAIGGAAAAAITAAAGIGGGGT 1550   1570	Oy 1558 CITGIGGCTGCTTTGGACCCCGTGCTCCTGCAGGACACTCTGTCTACGACCCTTGTG 1617	Oy 1618 GAGCALTCCGGAAGAGTITTTCGACTACAGTITGATGAATTCCAGATTGTCAGTAGTACA 1677	Oy 1678 CATGATGACACATCCTCATCTGGGACTTCCTAAATGATCCAGCTGCCCAAGCTGAACCC 1737
1570 TIGGACCCCCGTGCTCCTGCAGGGACACTCTGTCTACGGACCCTTGTGGAGCATTCCGGA 16	1630 AGASTITICGACIACAGITIGATGAATICCAGATIGTCAGIGGTCACAGAGACACA 	29 1690 AICCICATCIGGGACTICCIAAAIGATCACTGCCCAAGGTGAACCCCCCGTTCCCCT 1749	2y 1750 TCTCGAACATACACCTACATCTCCAGATAA 1779 	RESULT 4 25-09-832-161-15 . Germanne 15 annlication 18/0882161	Publication No. US20030166587A1 ; GENERAL INFORMATION: APPLICANT: Manning, Anthony M.	APPLICANT: Metculo, Frank APPLICANT: Ben-Neriah, Yinon APPLICANT: Ben-Veriah, Yinon APPLICANT: Davis, Matti	APPLICANT: TAYON, ITIS APPLICANT: Yaron, Avraham ITILE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF	FILE REFERENCE: 860098.427  CURRENT APPLICATION NUMBER: US/09/832,161  CURRENT PILING DATE: 2001-04-09  PRICE APPLICATION NUMBER: 0001-04-09	PRIOR FILING DATE: 1998: NUMBER OF SEQ ID NOS: 30 SOFTWARE: Patentin Ver: 250 Thus 15 Not 15	7	Ouery Match Quest Joan State March 41.1%; Score 883.4; DB 12; Length 4230; Alsk; Pred, No. 5.2e-272; Marches 1122: Conservative Or Micmatches 371; Indel C. Cons	TCCAGIAGATICGCCCAAGCAACGAAACTCTCAGCAAGC TCAGIAGATICGTCCAGAAAAAGCCATCAGAAGAAAAAAAAAA	358 GAAAAGGAACTGTGTGTCAAATACTTTGAGGAGTGAGTCAGATGAAGTTTT	418 GIGGAACATCITAIATCCCAANIGICACCAACAGGCCACATAAACTCGTATCTT 477  299 GIGGAACATCITAITTCCCAANIGICACTAACATCGCACATAAACTCGTATCTT 477  299 GIGGAACATCTTAITTCCAANIGICATAATCAACATGAACATCAATAAACTTAACAACAATAAAAAAAA	478 AAACCTATGTGGAGAGAGATTCATAACTGCTCTGCCAGCTCGGGGATTGCATACT	538 GCTGAGAACATTCTGTCATACTGGATGCCAAATCATAGGCTGCTGAACTTGTGTGC 59	598 AAGGATGGTACCAGTGACCTCTGATGGCATGCTGTGGAAGAGCTTATCGAGAATG 

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541 CGAGTGACCTCTGATGGCATGCTGTGGAAGCTTATCGAGAATGGTCAGGACAGAT 600
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Sequence 15, Application US/09764848

Setent No. US20020077270A1

GENERAL INFORMATION:

TAPLICANT: Rosen et al.

TITLE OF INVENTION: NUMBER: US/09/764,848

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper SOFTWARE: PatentIN Ver. 2.0

SOFTWARE: PatentIN Ver. 2.0

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LENGTH: 951
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larity 72.3%; Pred. No. 1.7e-128;
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                                                                                                                                                                                              APPLICANT: LEGRALOW, Pierre
APPLICANT: BENAROUS, Richard
APPLICANT: BLOT, Guillaume
APPLICANT: BLOT, Guillaume
APPLICANT: LASSOT, Irina
ITILE OF INVENTION: PROTEINS THAT INTERACT WITH BETA TrCP
FILE REFERENCE: B4117A
CURRENT APPLICATION NUMBER: US/10/023,530
CURRENT APPLICATION NUMBER: US/22
PRIOR APPLICATION NUMBER: G0/256,276
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                    RESULT 5
US-10-023-530-1
// Sequence 1, Application US/10023530
// Publication No. US20030007956A1
// GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: gene
; LOCATION: (1)...(657)
; OTHER INFORMATION: Beta TrCP
US-10-023-530-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 657; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1
LENGTH: 657
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Best Local
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REFIGURE DATE: 2000-09-21

REPLING DATE: 2000-09-21

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REPLING DATE: 2000-08-14

REPLING DATE: 2000-09-29

REPLING DATE: 2000-09-29

REPLING DATE: 2000-08-14

REPLING DATE: 2000-07-26
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FILING DATE: 2000-10-20
PR APPLICATION NUMBER: 60/244,617
PR FILING DATE: 2000-11-01
PR APPLICATION NUMBER: 60/225,268
PR FILING DATE: 2000-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/249,299
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/236,327
FILING DATE: 2000-09-29
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FILING DATE: 2000-10-02
APPLICATION NUMBER: 60/237,038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-10-02
APPLICATION NUMBER: 60/236,370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-10-02
APPLICATION NUMBER: 60/237,040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-10-20
APPLICATION UNDBER: 60/239,935
APLICATION UNDBER: 60/239,935
APPLICATION NUMBER: 60/239,937
                                FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/251,869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-09-29
APPLICATION NUMBER: 60/251,856
FILING DATE: 2000-12-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/251,868
FILING DATE: 2000-12-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLICATION NUMBER: 60/229,343
LING DATE: 2000-09-01
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APPLICATION NUMBER: 60/229,513
FILING DATE: 2000-09-05
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APPLICATION NUMBER: 60/237,037
                                                                                                                                                                                   APPLICATION NUMBER: 60/234,274
FILING DATE: 2000-09-21
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FILING DATE: 2000-09-25
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                                                                                              FILLING DATE: 2000-12-08
APPLICATION NUMBER: 60/235,834
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PRINCH PR
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   rrraaaaacagacccacag----arggcccrccaaarrcarrraraggccarrarac 607
                                                                                                                                                                                                                                                     608 CCAAAGATTATCCAGGATATAGAGACTATAGAATCTAACTGGCGGTGTGGACGACGACAAC 667
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                                                                 TICAAAAACAAACCICCIGACGGGAAIGCICCICCCAACICTITITAIAGAGCACTITAI
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Publication No. US20030175739A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ08C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US/10/222,020
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 10/116,016
PRIOR PLING DATE: 2002-04-05
PRIOR PLING DATE: 2001-01-17
PRIOR PLING DATE: 2001-01-17
PRIOR PLING DATE: 2000-01-31
PRIOR PLING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR PLING DATE: 2000-02-04
PRIOR PLING DATE: 2000-02-04
PRIOR PLING DATE: 2000-02-04
PRIOR PLING DATE: 2000-02-11
PRIOR PLING DATE: 2000-07-11
PRIOR PLING DATE: 2000-07-11
PRIOR PLING DATE: 2000-07-12
PRIOR PLING DATE: 2000-07-12
PRIOR PLING DATE: 2000-07-14
PRIOR PLING DATE: 2000-07-17
PRIOR PLING DATE: 2000-07-07
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APPLICATION NUMBER: 60/216,880
FILING DATE: 2000-07-07
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PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/241,808
PRIOR APPLICATION NUMBER: 60/241,808
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20 Query Match
Best Local Similarity 72.3%;
Matches 597; Conservative 134 374 598 434 554 278 1018 1078 358 418 254 478 538 629 718 838 868 728 787 gg ò qq ò Dp ઠે g ò ద à D ò 8 g ઠે Db ò ò ద ò à

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958 TIGGAAIGCAAGCGAATICTCACAGGCCAIACAGGITCAGICCTCTGTCTCCAGIAIGAI 1017
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                                                    608 CCAAAGATTATCCAGGATATAGAGACTATAGAATCTAACTGGCGGTGTGGACGACACAAC 667
                                                                                                                         668 TTGCAGAGGATTCAGTGCCGCTCTGAAAATAGTAAAGGTGTCTACTGTTTACAGTACGAT 727
                                                                                                                                                            GATCAGAAAATAGTAAGCGGCCTTCGAGACAACACAATCAAGATCTGGGATAAAAACACA 957
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                    CCTAAAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGAAGACATAGT
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APPLICATION NUMBER: US 09/608,408
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,906 GTGAAAGNTCTTAACACATTGATCCNCCCNATTGANGCTGATTTGC 951
                                                                                                                 GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION:
FILE REPERENCE: PIZGORIA:
CURRENT APPLICANTION NUMBER: US/10/116,016
CURRENT FILING DATE: 2002-04-05
Prior Application removed - See File Wrapper or Palm
NUMBER OF EQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
20.2%; Score 435.4; DB 14; Length
Best Local Similarity 72.3%; Pred. No. 1.7e-128;
Matches 597; Conservative 5; Mismatches 216; Indels
                                                                                                                                                                                                                                                                                                                                               VAME/KEY: misc feature

LOCATION: (883)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (913)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (931)

LOCATION: (935)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (935)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (941)
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                                                                                     Sequence 15, Application US/10116016
Publication No. US20030054379A1
                                                                                                                                                                                                                                                                                                 LENGTH: 951
TYPE: DNA
ORGANISM: Homo sapiens
                                                    RESULT 8
JS-10-116-016-15
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음 ò Op ò q ⋧ g ò g ò g ò 셤 ò d

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INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SIN TITLE OF INVENTION: GENE EXPRESSION ANALYSIS CURRENT FILLS REFERENCE: Accord.ca.x.1

CURRENT FILLNG DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILLNG DATE: 2000-05-26

PRIOR PELLING DATE: 2000-05-36

PRIOR PILLNG DATE: 2000-10-04

PRIOR PILLNG DATE: 2000-10-04

PRIOR PILLNG DATE: 2000-09-27

PRIOR PELLING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US 6/236,359

PRIOR FILLNG DATE: 2000-10-04

PRIOR PILLNG DATE: 2001-01-30

PRIOR PELLING DATE: 2001-01-30

PRIOR P
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278; Conservative
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TYPE: DNA
ORGANISM: Homo sapiens
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N LUNG, SIGNAL = 2.6

N HELA, SIGNAL = 2.8

N BOYT 4, SIGNAL = 2.8

N BONE MARROW, SIGNAL = 1.6

N PLACENTA, SIGNAL = 1.6

N HERRY, SIGNAL = 1.9

N BRAIN, SIGNAL = 1.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADULT LIVER, SIGNAL = 1.8 FETAL LIVER, SIGNAL = 1.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION WHRER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
LENGH: 479
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SED IN HBL100,
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Patent No. US20020048763A1
PAPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
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OTHER INPORMATION: MY
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Matches 359;
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1027 ATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGATGTAAATACAGGTGAAATG 1086
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NN: EXPRESSED IN HELLO, SIGNAL = 2.6

NN: EXPRESSED IN HELLA, SIGNAL = 2.6

NN: EXPRESSED IN HELLA, SIGNAL = 2.6

NN: EXPRESSED IN BT44, SIGNAL = 0.75

NN: EXPRESSED IN DOUE MARKOW, SIGNAL = 1.6

NN: EXPRESSED IN PLACENTA, SIGNAL = 1.9

NN: EXPRESSED IN HEART, SIGNAL = 1.9

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7

NN: EXPRESSED IN SURJECT LIVER 3.00e-162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 208.4; DB 9; Length 370;
Pred. No. 8e-56;
0; Mismatches 91; Indels 5
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 19492
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Sequence 4953, Application US/10029386
Publication No. US20030194704A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-10-029-386-18709/c
                                                                                                                                                                                                                                                      SEQ ID NO 4953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1117
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                                                                                                                                      1207 ATTACCCTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGTCAATGTTGTAGACTTTGAT 1266
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                                                            1147 ATGGTGACCTGCTCCAAAGATCGTTCCATTGCTGTATGGGATATGGCCTCCCCAACTGAC 1206
                                                                                                                                                                                                                 1267 GACAAGTACATTGTTGTGGGTGTGTGGGATAGAACTATAAAGGTATGGAACACAGTACT 1326
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249 ATGGTGACCTGTTCCAAGGACCGCTCCATTGCTGTGGGACATGGCTTCTGCGACCGAT 190
                                                                                                                                                                                                                                                                                                                               15
                                                                                                                                                                                                                                                   129 GAGAAATACATCGTGTCTGCCTCTGGTGACAGGACCATCAAAGTCTGGAGCATGAGCACC 70
                                                                                                                                                                    189 Arcacttracgregrercregrigicalcactercreacterateactrigation
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; LOCATION: (261)

; OTHER INFORMATION: unsure at all n locations

; OTHER INFORMATION: Clone ID: 13-LIB3058-049-Q1-K1-D1

US-09-960-352-2934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.4%; Score 180.2; DB 10; 93.1%; Pred. No. 8.3e-47; ive 0; Mismatches 14;
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GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT Tao, Nengbing
APPLICANT Tao, Nengbing
APPLICANT BYALT, JOHN CALL
TILLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECU
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECU
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECU
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECU
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT PILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2934, Application US/09960352 Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                     1387 GACAGGCTGGTAGT 1400
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Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          GATGGGCTGGTTGT
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US-10-029-386-4953/c
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JS-09-960-352-2934
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                                                                                                                                                                                                                                                                                    Sequence 18709, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Penn, Sharron G.

APPLICANT: Hansel, David R.

APPLICANT: Hansel, David R.

APPLICANT: Hansel, David R.

APPLICANT: Hansel, David R.

APPLICANT: Penn, Sharron G.

APPLICANT: Penn, Sharron G.

APPLICANT: Penn, Sharron G.

APPLICANT: Penn, Sharron G.

APPLICANT: Hansel, David R.

APPLICANT: Bank BENGE SEND ANALYSIS TWO

FILLE REFERENCE: AEOMICA-X-2

CURRENT APPLICANTON: WIMBER: US/10/029,386

CURRENT FILLING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 18709

LENGTH: 250

TYPE: DNA
PUBLICATION NO. US2003019470441

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: HARZEL, David K.
APPLICANT: HARZEL, David K.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION UNMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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OTHER INPORMATION: EXPRESEED IN ADULT LIVER, SIGNAL = 2.5

OTHER INFORMATION: EXPRESEED IN HEART, SIGNAL = 4.5

OTHER INFORMATION: EXPRESEED IN BRAIN, SIGNAL = 3

OTHER INFORMATION: EXPRESEED IN BONE MARROW, SIGNAL = 1.6

OTHER INFORMATION: EXPRESEED IN DONE MARROW, SIGNAL = 2.6

OTHER INFORMATION: EXPRESEED IN PLACENTA, SIGNAL = 4.1

OTHER INFORMATION: SIGNAL = 4.1

OTHER INFORMATION: STREAM ADULT: QUARALUE 0.000+40

OTHER INFORMATION: EST_HUMAN HIT: BI088274.1, EVALUE 0.000+00

US-10-029-386-4953
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78.0%; Pred. No. 1.2e-42;
rative 0; Mismatches 57; Indels
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GCAGTCCGCTGTGTTCAATATGATGGCAGGAGGGTTGTTAGTGGAGCATATGATTTTATG 1065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1123 CACTIGGGIIICAAIAAIGGCAIGAIGGIGACCIGCICCAAAGAICGIICCAIIGCIGIA 1182
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GNGAATGATTGGAACTTTGGAAGGTCCCCTCCTCCTCCTCTCCCTTTCACCTCTGCACCTANT 174
                                                                                                                                      TITICCCATIGGITCCAGACAAAGGIGACTIAIAAAIAIATTTAGIGITTIGCCAGAA 2143
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                                                                                                                                                                                  Query Match 5.8%; Score 124.2; DB 12; Length 1620; Best Local Similarity 50.2%; Pred. No. 2.7e-28; Matches 340; Conservative 0; Mismatches 328; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Reed, Steven
APPLICANT: Reed, Steven
APPLICANT: Strohmaier, Heimo
APPLICANT: Strohmaier, Heimo
APPLICANT: Strohmaier, Gharles
APPLICANT: Spruck, Charles
TITLE OF INVENTION: HCDC4 MODULATES CYCLIN E DEGRADATION
FILE REFERENCE: TSRI 779.2
CURRENT APPLICATION NUMBER: US/10/245,618
CURRENT FILING DATE: 2002-09-16
RRIOR APPLICATION NUMBER: US 60/404,116
PRIOR PILING DATE: 2002-08-15
PRIOR PILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 1620
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/10245618; Publication No. US20030143582A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-10-245-618-13
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                                  FEATURE:
OTHER INFORMATION: MAP TO ACO11387.4
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.5
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3
OTHER INFORMATION: EXPRESSED IN UNGW. SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN DONE MARROW, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.1
OTHER INFORMATION: STRINGSOG497, EVALUE 0.00e+00
OTHER INFORMATION: WI HIT: G116306497, EVALUE 5.00e+43
US-10-029-386-18709
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Sequence 15756, Application US/0991895

Publication No. US20030073623A1

GENERAL IMPRORMATION:

APPLICANT: HYSSG, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT.

TITLE OF INVENTION: RROW VARIOUS CDNA LIBRARIES

FILE REFERENCE: 2041.-756

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: PSALSEQ for Windows Version 3.0

LENGTH: 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.6%; Score 162.6; DB 1:
Best Local Similarity 78.3%; Pred. No. 3.1e-41;
Matches 195; Conservative 0; Mismatches 54
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NAMB/KES: misc feature
LOCATION: (1)...(475)
OTHER INFORMATION: n = A,T,C or () US-09-918-995-15756
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ORGANISM: Homo sapiens
    ORGANISM: Homo sapiens
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Search completed: October 22, 2003, 23:59:06 Job time: 578 secs

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; Sequence 2, Application US/09172841; Patent No. 6232081; GENERAL INFORMATION:
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Best Local Similarity 99.2%;
Matches 125; Conservative
        TYPE: DNA
ORGANISM: Homo sapiens
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RESULT 1
US-09-172-841-2
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Sequence 2, Appli
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6458.606 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Sequence 1, Ag
Sequence 8, Ag
Sequence 8, Ag
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Sequence 17
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Sequence 3
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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4 US-08-951-621-2

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2 US-08-99-73-1

1 US-08-21-14-14

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1 US-08-21-16-14

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1 US-08-21-16-14

1 US-08-21-16-14

1 US-08-64-5-11

1 US-08-64-5-11

1 US-08-65-18-11

1 US-08-65-18-11

2 US-09-156-18-11

4 US-09-962-665-8

4 US-09-962-665-8

4 US-09-962-665-8

4 US-09-962-61-18-11

US-09-18-148-11

US-09-18-14-145-2

US-09-18-14-145-2

US-09-18-13-14-13
                                                                                                                                                                     otal number of hits satisfying chosen parameters:
                                                                                                                                                       569978 seqs, 220691566 residues
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                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         nucleic - nucleic search, using sw model
                                                        October 22, 2003, 18:30:59
                                                                                                                            IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                       inimum DB seq length: 0 taximum DB seq length: 2000000000
                                                                                          US-09-601-168B-1
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Sequence 1, Appli
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Sequence 24, Appli
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Sequence 11, Appli
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Sequence 336, Appli
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Pred. No. 9.4e-31;
0; Mismatches 1;
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US-08-951-621-2
Sequence 2, Application US/08951621
Fatent No. 6573094
Patent NIFORMATION:
APPLICANT: HARPER, JEFFREY W.
APPLICANT: HARPER, STEPHEN J.
TITLE OF INVENTION: F-BOX GENES AND PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
US-09-184-445-1

US-09-357-206A-9

US-09-357-206A-9

US-08-014-999-5-1

US-08-016-421B-1

US-08-013-553-10

US-08-013-553-10

US-09-032-742-3

US-09-032-742-2

US-09-032-742-2

US-09-032-742-25

US-09-033-3336-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Harper, Jeffrey W.
APPLICANT: Eldede, Stephen J.
TITLE OF INVENTION: F-BOX PROTEINS AND GENES
FILE REFERENCE: BCM-03510
CURRENT APPLICATION WUMBER: 08/09/172,841
CURRENT PILING DATE: 1998-10-15
EARLIER APPLICATION NUMBER: 08/951,621
EARLIER FILING DATE: 1997-10-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
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1781 GTATATCTGGTCAATATTTATTTAGTGGTTCAAATGATAAAACTATCAAGGTTTGGGATT 1840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1019 AGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGGATGTAAATACAG 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1610 TAAGATGTATTTTACTTTGGAGGGTCATGATAACCTGTCCATACGGTTCTATTGAATG 1669
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3.8%; Score 82.2; DB 4; Length 2
Best Local Similarity 47.4%; Pred. No. 4.4e-16;
Matches 286; Conservative 0; Mismatches 308; Indels
                                           ATTORNEY AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION UNDRER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5800
TELEPHONE: 201-483-1684
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2237 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: CDN
HYPOTHETICAL: NO
  FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1559 TTG 1561
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US-08-899-578-1
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Patent No. 6346406
GENERAL INFORMATION
APPLICANT: Ryazanov, Alexey G.
APPLICANT: Hail, William N.
APPLICANT: Hail, William N.
APPLICANT: Bavia', Karen S.
TITLE OF INVENTION: ELONGATION FACTOR-2 KINASE (EF-2 KINASE)
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: #11 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.8%; Score 124.4; DB 4; Length 126; 99.2%; Pred. No. 9.4e-31; ive 0; Mismatches 1; Indels 0
                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IGN PC compatible
COMPUTER: IGN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,621
FILING DATE: 16-OCT-1997
CLASSIFICATION: 536
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,999
                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION UNDRER: 38,230
REPRENCE/DOCKET NUMBER: BCM-02999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                   California
. United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/914,999
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
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MEDIUM TYPE: Floppy disk
MEDIUMTYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TYPE: nucleic acid
STRANDEDNESS: double
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San Francisco
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STATE: New Jersey
COUNTRY: USA
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Matches 125; Conserv
                                                                          94104
                     STATE: C. COUNTRY:
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JS-08-914-999-7
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us-09-601-168b-1.rni

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STRANDEDNESS:
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; LOCATION:
US-08-283-917-8
                                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.1%; Score 67.2; DB 3; Length 2481;
50.6%; Pred. No. 3.9e-11;
tive 0; Mismatches 158; Indels 0
                                                                                                                                                                                                                                                                                       ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,578
FILING DATE: 24-JUL-1997
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REFERENCE/POCKET NUMBER: 0575/53200/JPW/AKC
TELEPHONE: (212) 278-0400
TELEPAK: (212) 278-0400
TELEPAK: (212) 278-055
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
--NAGTH: 2481 base pairs
                                        APPLICANT: Greenwald, Iva
APPLICANT: Greenwald, Iva
APPLICANT: Hubbard, E. Jane
IITLE OF INVENTION: SEL-10 AND USES THEREOF
CORRESPONDENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1573 GACCCCCCGTGCTCCTGCAGG 1592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2481 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.6
Matches 162; Conservative
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91..1854
                                                                                                                                                                                                              CITY: New York
STATE: New York
COUNTRY: U.S.A.
Patent No. 6087153
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JS-08-899-578-1
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RESULT 5 |US-08-283-917-8 , Sequence 8, Application US/08283917

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1364 Traagcrardagartrircagagcrrrgaargcarcaagcardcardgcardaca---c 1420
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GENERAL INFORMATION:
APPLICANT: ADACHI, HIDEKI
APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: NUTU, KEIZO
APPLICANT: ARAI, HIROYUKI
TITLE OF INVENTION: OXIDIZED PHOPHOLIPID DEGRADING ENZYME
TITLE OF INVENTION: AND GENE THEREOF
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSE:
ADDRESSEE: ADBLOW, SPITAR, MCCLELLAND, MAIER &
ADDRESSEE: NEUSTADI, P.C.
                                                                                                                                                                                                                                                                                                                                                     1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                         CITY: Arington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 2202
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC Compatible
SOFTWARE: PAPELICATION NUMBER: US/08/283,917
FILING DATE: 03-AUG.1994
CLASSIFICATION NUMBER: JP 209943/1993
FILING DATE: 03-AUG.1993
ATTORNEY/AGENT INFORMATION:
NAMME: Oblon No. 5849557man F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 2292-030-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703) 413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2085 harr
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nucleic acid
IDEDNESS: unknown
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MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Bos taurus
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1001 TCTGTCTCCAGTATGATGAGAGAGTGATCATAACAGGATCATCGGATTCCACGGTCAGAG 1060
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                                                                                                                                                                                                                                                                                                                                                                             1061 TGTGGGATGTAAATACAGGTGAAATGCTAAACACGTTGATTCACCATTGTGAAGCAGTTC
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                                                                                                                                                                                                                           15; Gaps
                                                                                                                                                                  Score 50.8; DB 2; Length 2085;
Pred. No. 8.2e-06;
0; Mismatches 277; Indels 15
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COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OCMPUTER: FROM PC compatible
OFFWATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DCRNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                     Query Match
Best Local Similarity 47.3%;
Matches 262; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1529 CCTATGATGGAAAA 1542
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              Bos taurus
                                                          CDS
844..2073
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        ORGANISM:
                                                        ), NAME/KEY;
, LOCATION;
US-08-961-716-8
                                                                                                                                                                  Query Match
                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                          1661 GAGAACATGAGCATGTGGTAGAATGCATTTCCTGGGCTCCTGAAAGCTCATATTCTTCCA 1720
                                                        1295 ATAGAACTATAAAGGTATGGAACACAAGTACTTGTGAATTTGTAAGGACCTTAAATGGAC 1354
1421 ACAATGTTTCTTCAGTAGCCATCATGCCCAATGGAGATCATAGTGTGTCTGCCTCAAGGG 1480
                                                                                                          1481 ATAAAACTATAAAAATGTGGGAAGTGCAAACTGGCTACTGTGTGAAGACATTCACAGGAC
                                                                                                                                                          ACAAACGAGGCATTGCCTTTTGCAGTACAGGGA-----CAGGCTGGTAGTGAGTGGCT
                                                                                                                                                                                                               1541 ACAGAGAATGGGTACGTATGGTGCGGCCAAATCAAGACGGCACTCTGATAGCCAGCTGTT
                                                                                                                                                                                                                                                                     1409 CATCTGACAACACTATCAGATTATGGGACATAGAATGTGGTGCATGTTTACGAGTGTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: INOUT:
APPLICANT: NAL, HIROYUKI
TITLE OF INVENTION: OXIDIZED PHOPHOLIPID DEGRADING ENZYME
TITLE OF INVENTION: AND GENE THEREOF
NUMBER OF SEQUENCES: 31
CARRESEDE: OBLOW, SPIVAK, MCCLELLAND, MAIER &
ADDRESSE: SPIVAK, MCCLELLAND, MAIER &
ADDRESSE: MEUSTADT, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
FILING DATE:
APPLICATION DATA:
APPLICATION NUMBER: US 08/283,917
FILING DATE: 03-AUG-1994
APPLICATION NUMBER: D 209943/1993
ATTORNEY AGENT INFORMATION:
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 229-030-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAN: (703) 413-3000
TELEFAN: (703) 413-4000
TELEFAN: 248852 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LEMCTH: 2085 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/961,71
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MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/08961716
Patent No. 5880272
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1529 CCTATGATGGAAAA 1542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1721 réferènageadea 1734
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: NEUST
STREET: 1755 S. C
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-08-961-716-8
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1325 CTTGTGAATTTGTAAGGACCTTAAATGGACACAAGGAGGCATTGCCTGTTTGCAGTA-- 1382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1383 ----CAGGGACAGGCTGGTAGTGAGTGGCTCATCTGACACACTATCAGATTATGGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1265 ATGACAAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTATGGAACACAAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1625 ATTCTAATTATGTTGCTACGGGCTCTGCAGACAGAACTGTGCGGCTCTGGGACGTCCTGA
   TATA-BINDING PROTEIN ASSOCIATED FACTORS, NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
2.2%; Score 47.8; DB 1; Length 215
Best Local Similarity 52.6%; Pred. No. 8e-05;
Matches 131; Conservative 0; Mismatches 112; Indels
                                                                                                                           ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                      COMPUTER EALCABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPTITE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,582
FILING DATE: 28-JAN-1994
CLASSIFICATION NUMBER: US/08/188,582
ATTONINY/AGENT INFORMATION:
NAME: COMMAN: Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/POCKET NUMBER: 36,627
REFERENCE/POCKET NUMBER: 36,627
RELEFEX: (415) 781-1989
TELEFEX: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
US-08-646-715-17
US-08-646-715-17
Sequence 17, Application US/08646715
Patent No. 5637686
; GENERAL INFORMATION:
APPLICANT: Tjian, Robert
APPLICANT: Comai. Lucio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tjian, Robert
Comai, Lucio
Dynlact, Brian D.
Hoey, Timothy
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TITLE OF INVENTION: TP
TITLE OF INVENTION: NI
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) NAME/KEY: CDS
) LOCATION: 1...
US-08-188-582-17
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APPLICANT:
APPLICANT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             826 GGAAGACAIAGITIACAGAGAATICACIGCCGAAGIGAAACAAGCAAAGGAGITIACIGI 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           586 GAACTIGIGCAAGGAAIGGIACCGAGIGACCICIGAIGGCAIGCIGIGGAAGAAGCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           766 AGAGCACTITATCCTAAAATTATACAAGACATTGAGACAATAGAATCTAATTGGAGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:

CLASSIFICATION 1435
PRIOR APPLICATION 1435
PRIOR APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT: Scephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)838-4109
                                        US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang, Edith
Weinzierl, Robert O.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/08188582
Patent No. 5534410
GENERAL INFORMATION:
APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Comai, Lucio
Dynlact, Brian D.
Hoey, Timothy
Ruppert, Siegfried
Tanese, Naoko
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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US-08-232-463-14
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Best Local Similarity
Matches 20; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
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| US-08-188-582-17
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1325 CITGIGAATITGTAAGGACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGCAGTA-- 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1439 TAGAATGTGGTGCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTC 1498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1745 CTCCCAATGGGAGATTCCTGGCTACAGGAGCAACAGATGGCAGGGGGGTGCTTCTTTGGGATA 1804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1265 ATGACAAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTATGGAACACAAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
         APPLICANT: Tanese, Nacoc APPLICANT: Wang, Edith APPLICANT: Wang, Edith APPLICANT: Wang, Edith APPLICANT: Wang, Edith APPLICANT: Weinzierl, Robert O.J., TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS, TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS, TITLE OF INVENTION: TATA-BINDING PROTEIC ACIDS ENCODING TAFS AND METHODS OF USE NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESSE: FLERR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.2%; Score 47.8; DB 1; Length 2152; Best Local Similarity 52.6%; Pred. No. 8e-05; Matches 131; Conservative 0; Mismatches 112; Indels 6
                                                                                                                                                                                                                                                                                ZIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTLM Release #1.0, Version #1.25
CURRATY APPLICATION DATA:
APPLICATION NUMBER: US/08/646,715
FILING DATE: 09 PAXY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 105 08/188,582
PILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
RGISTRATION NUMBER: 36,627
REPERBNCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECHONE: (415) 781-1989
TELEFRONE: (415) 398-3249
Ruppert, Siegfried
Tanese, Naoko
Wang, Edith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2152 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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; LOCATION: 1...2
US-08-646-715-17
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RESULT 10 US-08-232-463-14

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1954 TCGGCCCAGGACGGTCTACTCAGCACAACTGACTGCTTCAGTGCTGCTATCAGAAGATGT 2013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1774 AGATAAATAACCATACACTGACCTCATACTTGCCCAGGACCCATTAAAGTTGCGGTATTT 1833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1834 AACGTATCTGCCAATACCAGGATGAGCAACAACAGTAACAATCAAACTACTGCCCAGTTT 1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1714 GATCCAGCTGCCCAAGCTGAACCCCCCCCTTCTCCAACATACACCTACATCTCC 1773
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3.6%; Pred. No. 0.076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
1.9%; Score 39.8; DB 1; Length 7
Best Local Similarity 3.6%; Pred. No. 0.076;
Matches 14; Conservative 210; Mismatches 167; Indels
                                                                                                                                                                                                                                                                       STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAINE:
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAMES: US/08/232,463
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
CORRESPONDENCE: 52
CORRESPONDENCE ADDRESS:
ADDRESSEB: FOLEY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION, 435
PRIOR APPLICATION OWEN:
APPLICATION NUMBER: US/07/935,313
PILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REPRENCE/DOCKET NUMBER: 30472/114 IMM
TELECOMMUNICATION HORMATION:
TELECOMMUNICATION HORMATION:
TELECOMMUNICATION HORMATION:
                                                                                                                                                                                                   SSEE: Foley & Lardner I: 1800 Diagonal Road, Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (703)836-9300
(703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: line
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CITY: AJ
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ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/738,367
                                                                                                                                                                                                                                                                                                                                  B: Genetics Institute,
87 CambridgePark Drive
                           Sequence 1, Application US/08738367
Patent No. 5827688
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08738367
Patent No. 5827688
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: MCCOy, John
APPLICANT: LaVallie, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BTOWN, SCOCK A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 433 base pairs
                                                                                                                   McCoy, John
LaVallie, Edward
Racie, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 51.4%
whiches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                    Massachusetts
                                                                                                                                                                                                                                                                                                                                           STREET: 8/ CAMbridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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US-08-738-367-6
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1396 GIAGIGAGIGGCICAICIGACAACACIAICAGAITAIGGGACAIAGAAIGIGGIGCAIGI 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 GTCATAACTTCTTCATGGGATAATAATGTCTATTTTTATTCCATAGCATTTGGAAGACGC 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 CAGGACACGTTAATGGGACATGATGATGCTGTTAGTAAGATCTGTTGGCATGACAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: McCoy, John
APPLICANT: Racie, Lisa
APPLICANT: Racie, Lisa
APPLICANT: Treacy, Maurice
APPLICANT: Frans, Cheryl
APPLICANT: Spanis, Cheryl
APPLICANT: Spanis, Cheryl
APPLICANT: Spanis, Cheryl
APPLICANT: Bowman, Michael
ITILE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: BROODING THEM
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSES ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.8%; Score 38.6; DB 1; Length 433;
51.4%; Pred. No. 0.028;
tive 0; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/664,596B
                                                                              1412 YYYYYYYYYYYYYYYYYYYYYYYGTACCAAA 1442
                                                2074 CIGCACCIAGITITITCCCATIGGITCCAGA 2104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Genetics Institute, Inc
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                            ESULT 11
78-08-664-596B-1
Sequence 1, Application US/08664596B
Patent No. 5807703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 499-8224
TELEPAX: (617) 876-8821
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 433 base pairs
nucleic acid
EDNESS: double
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Best Local Similarity 51,4<sup>5</sup>
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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CITY: C
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RESULT

1396 GTAGTGAGTGGCTCATCTGACACACTATCAGATTATGGGACATAGAATGTGGTGCATGT 1455 107 GTCATAACTTCTTCATGGGATAATAATGTCTATTTTTATTCCATAGCATTTGGAAGACGC 166 167 CAGGACACGTTAATGGGACATGATGATGCTGTTAGTAAGATCTGTTGGCATGACAGCGG 226 1456 ITACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTAITCGATTTGAIAACAAGAGG 0; Gaps 1516 ATAGTCAGTGGGGCCTATGATGGAAAATTAAAGTGTGGGGATCTTGTGGCTGC 1568 227 CTATATICTGCATCGTGGGACTCTACAGTGAAGGTGTGGTCTGGTGTTCCTGC 279 Score 38.6; DB 1; Length 433; Pred. No. 0.028; 0; Mismatches 84; Indels APPLICANT: Racie, Lisa
APPLICANT: Racie, Lisa
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurica
APPLICANT: Treacy, Maurica
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLECTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES:
CORRESPONDBACE ADDRESS:
ADDRESSEE: Genetics Institute, Inc. Jacobs, Kenneth MCCoy, John LaVallie, Edward Racie, Lisa Merberg, David Treacy, Maurice APPLICANT: APPLICANT: APPLICANT:

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Gaps

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1396 GTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACATAGAATGTGGGTGCATGT 1455
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                                                                                                                                                                                                                                                                                                          1456 ITACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTCGATTTGATAACAAGAGG 1515
                                                                                                                                                                                                                                                                                                                                                                               2131 CAGGACACGITAATGGGACATGATGATGCTGTTAGTAAGATCTGTTGGCATGACAGG 2190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1242 IGCIGICAAIGIIGIAGACIIIGAIGACAAGIACAIIGIIICIGCAICIGGGAIAGAAC 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1302 TATAAAGGTATGGAACACAAGTACTTGTGAATTTGTAAGGACCTTAAATGGACACAAAACG 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1516 ATAGTCAGTGGGGCCTATGAAAATTAAAGTGTGGGGATCTTGTGGCTGC 1568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2191 ciararrergearegiogaereraeagigaaggiergeregerergerefiee 2243
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                          Length 3380;
                   1.8%; Score 38.6; DB 2; Length 33
51.4%; Pred. No. 0.11;
cive 0; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Drmanac, Radoje T.
ITILE OF INVENTION: Polypeptides
ITILE OF INVENTION: Polypeptides
ITILE OF INVENTION: Polypeptides
ITILE OF INVENTION: Polypeptides
CURRENT APPLICATION NUMBER: US/99/620,312D
CURRENT APPLICATION NUMBER: US/99/620,312P
CURRENT APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/489,725
PRIOR APPLICATION NU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1362 AGGCATTGCCTGTTTGCAGTACAG 1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1051, Application US/09620312D
Patent No. 6569662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.7%;
               Query Match
Best Local Similarity 51.4%
Matches 89; Conservative
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Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang, Zhiwei
John Tillinghast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 53.58
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
Ma, Yunging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang, Y. Tom
Liu, Chenghua
Asundi, Vinod
Zhang, Jie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1)..(7518)
US-09-620-312D-1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -09-620-312D-1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 Grcahakerrerrearggarakarahargretarrintarrecarakgearringaagaege 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1396 GTAGTGAGTGGCTCATCTGACACACTATCAGATTATGGGACATAGAATGTGGTGCATGT
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APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLECTIDES
TITLE OF INVENTION: BUCODING THEM
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute, Inc.
STREET: 87 Cambridge-Park Drive
CITY: Cambridge
STREET: Massachusetts
CUNTX: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
COMPUTER: ISM PC COMPATIBLE
COMPUTER: ISM PC COMPATIBLE
COMPATIBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPATIBLE
COMPATIBLE FORM:
MEDIUM TYPE: Floppy disk
COMPATIBLE SYSTEM: PC-DOS/MS-DOS
COMPATIBLE SYSTEM: PC-DOS/MS-DOS
COMPATIBLE SYSTEM: PC-DOS/MS-DOS
COMPATIBLE SYSTEM: PC-DOS/MS-DOS
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Batent No. 5962671
GENERAL INFORMATION:
APPLICANT: Baker, Brenda F.
APPLICANT: COWSET, LOX M.
TITLE COPINSTION: ANJERNSE MODULATION OF FAN EXPRESSION
FILE REFERENCE: RTS-0009
CURRENT PAPLICATION NUMBER: US/09/156,425B
CURRENT PILLING DATE: 199-09-18
NUMBER OF SEQ ID NOS: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin network of the Current Application NUMBER: US/08/738,367 FILING DATE: CLASSIFICATION NUMBER: US/08/738,367 FILING DATE: CLASSIFICATION: 514 ATTONEY ACTONEY ACTONEY ACTONEY ACTONEY ACTONEY ACTONEY ACTONEY OF TELEFONNICATION INFORMATION: TELEFONNICATION FOR SEQ ID NO: 5 SEQUENCE CHARACTERISTICS: LENGTH: 733 base pairs TYPE: nucleic acid TYPE: nucleic acid TYPE: nucleic acid TYPE: nucleic acid TYPE: ACTONEY I: near
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , NAME/KEY: CDS
, LOCATION: (23)..(2766)
JS-09-156-425-1
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MOLECULE TYPE:
US-08-738-367-6
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LENGTH: 3380
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US-09-156-425-1
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Gaps

0;

1683 ATCAATTACATCTTTACAGTTTAG 1706

Search completed: October 22, 2003, 21:59:58
Job time : 150 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

DM protein - protein search, using sw model

Run on: October 22, 2003, 10:15:16 ; Search time 43 Seconds

(without alignments)

1272.558 Million cell updates/sec

Title: US-09-601-168B-2

Perfect score: 3034
Sequence: 1 MDPAEAVLQEXALKFWNSSE.......PAAQAEPPRSPSRTYTYISR 569

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308
```

mum DB seq length: 0

Minimum DB seg length: 0 Maximum DB seg length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :  $\frac{\text{Distillul factor}}{\text{Distilly}}$  2:  $\frac{\text{Dist}}{\text{Dist}}$ ; 4:  $\frac{\text{Dist}}{\text{Dist}}$ ; 4:  $\frac{\text{Dist}}{\text{Dist}}$ ;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

beta-transducin re
hypothetical prote
WD-repeat protein
probable sulfur me
MET30 protein ye
sulfur controllerhypothetical trp-a
beta transducin-li
WD repeat protein
WD 40 repeat prote platelet-activation hypothetical prote hypothetical WD-re myosin-heavy-chain hypothetical prote WD-repeat protein WD-40 repeat regul cell division cont P-box/WD-repeat pr WD-Yepeat protein WD-40 repeat prote WD-40 repeat protein WD-70 repeat protein WD-40 repeat protein serine/threonine k hypothetical prote LIS-1 proteín - hu Description SUMMARIES T38932 S49932 T46660 T22703 S62507 T18521 T45136 AE1810 S56245 T43557 AC1842 AC2239 AE1861 % Query Match Length DB 2597 1635.5 690 590.5 531.55 531.55 513.52 513.55 455.55 453.3 396.5 378.5 375 374 373.5 373.5 361.5 Result No. 

2 AG1889	0.00	2 Appet unit-C	0 + 0 0 t 0 0 t 0 0 t 4 7	05004 7	22001111	5 2 T19266 hypothetical prote	7	2 AG2375	2 T51507	2 \$76086		2 AH2154	2 \$33263	2 T03818	2 AF1890	2 AI2099	2 T41148	2 AG1837
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## ALIGNMENTS

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C.Species: Schizosaccharomyces pombe
C.Species: Schizosaccharomyces pombe
C.Species: Schizosaccharomyces pombe
C.Species: Og-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 02-Sep-2000
C.Accession: TS021
C.Accession: TS021
C.Accession: TS021
C.Accession: TS021
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated WD repeat proteins; WD repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLSKEGVVAVYNHVRSLLFTDFTEVFF----EEVSLRVFSYLDQLDLCKCKLMSKRWKRL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 QFIF-----DSNGRPLLNWSYLY----KEHAHLDSNWRHGRFLVSTFNNPSIRFPADQDF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218 RATLDSVYCVQYDDEIMVSGSKDRTVSVMDVNSRFILYKLYGHSGSVLCLDFCRRRNLLV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGSSDSTIIMDWQNRRPLKVYFGHTDNVLGVVVSENYIISSSRDHTARVWRLDATSPAE 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 -ETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDER--VII 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVW--DMASPTD 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380 ITLRRVLVGHRAAVNVVDFDDK--YIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             338 ACM-HVLRGHLASVNSVQYSSKTGLIVTASSDRTLRTWDITTGHCIRIIHAHQRGIACAQ 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438 YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL 497
                     RESULT 3
TO2211
WD-repeat protein [imported] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 OMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 TSDGMLWKKLI-----ERMVRTDSLWRG-------LAERRGWG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 LEDPGIWKALYMQKGWPVNENVLNEFEAWRRTHKFPQPRFENFLKQQNIIGPYGTMFLPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 KNVVSKVSDLTSCSDFSTSSPVPCLNPLS-------HBNNRIDLIRDLIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  498 VAALDPRAPAGTLCLRTLVEH-----SGRVFRLQFDEFQIVSSSHDDTILIWDF 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 QYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRS
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A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:K10B2.1
A;Introns: 78/3; 125/1; 183/2; 281/3; 404/3; 551/3; 668/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 DYSCSRILSGHIGSVLCLQYDNRVIISGSSDATVRVWDVETGECIKTLIHHCEAVLHLRF 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          416 NISTCEFVRILNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRC 475
YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55
                                                                                                                                                                                                                                                                        hypothetical protein K10B2.1 - Caenorhabditis elegans
CjSpecies: Caenorhabditis elegans
CjSpecies: Caenorhabditis elegans
CjSpecies: 20.8ep-1999 #sequence_revision 20.8ep-1999 #text_change 20.8ep-1999
CjAccession: T16607
RjMiller, N.
Submitted to the EMBL Data Library, June 1995
AjDescription: The sequence of C. elegans cosmid K10B2.
AjReference number: Z18545
AjAccession: T16607
AjStatus: preliminary, translated from GB/EMBL/DDBJ
AjResidues: DNA
AjResidues: 1-701 <MIL>
                                   403 YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 IRPMLORDFISNLPA----HLVELILFNVNSDSLKSCEEVSTSWRCALARGOHWKKLIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YPKIIRDIHNIDNNWKRGNYKMTRINCQSENSKGYYCLQYDDDKIVSGLRDNTIKIWDRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 SMIVPKOR----KLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 LKPMLORDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 NVRSDSLWWGLSEKRQWDKFLNISRDMSVRRICEKFNYDVNIKRDKLDQLILMHVFYSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVW
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                                                                                                                                   VAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 RKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLAN-
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Cispecies: Neurospora crassa
Cibate: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-Jul-2000
Cibate: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-Jul-2000
Cibate: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-Jul-2000
Rikumar, A.; Paietta, J.V.
Rikumar, A.; Paietta, J.V.
A; Rumar, A.; Paietta, J.V.
A; Fille: The sulfur controller-2 negative regulatory gene of Neurospora crassa encodes a A; Reference number: Z23121; MUID:95241499; PMID:7724564
A; Accession: T4666
A; A; Accession: T4666
A; A; Callaninary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERR- 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---GWGQYLFKNK-----PPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQ 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92 ASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPAR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 RIHCRSETSK----GVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQ 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 PNCGWGLPLLHMKRARIQQNSTGSSSNADIQTQTTRPWKVIYRERFKVESNWRKG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     410 ESRICYTLR----GHTEWVNCVKLHPKSFSCFSCSDDTTIRMWDIRTNSCLKVFRGHVGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        526 LSCGLDNTIKLWDVKTGKCIRTQFGHVEGVWDIAADNFRIISGSHDGSIKVWDLQSG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPEYNFTKFCYRHNPDIQFSPTHTACYKQDLKRTQEINANIAKLPLQEQSDIHHIISKYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375 ASPIDITLRRVLVGHRAAVNVVDFDDKYI--VSASGDRIIKVMNTSICEFVRILNGH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           466 VQKIIPLTIKDVENLATDNTSDGSSPQDDPTMTDGADESDTPSNEQETVLDENIPYPTHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----DNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 IPEKNSLROTYNSCARLCLN-QETVCLASTAMKTENCVAK-TKLANGTSSMIVPKQRKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL: U17251; NID: 9806757; PIDN: AAA68968.1; PID: 9806758
                                                                                                                                                                                                                                                                                                                                                 tch 18.0%; Score 545; DB 2; Length 640; al Similarity 28.9%; Pred. No. 3.2e-34; 167; Conservative 85; Mismatches 202; Indels 124;
                                                                                                                         repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sulfur controller-2 protein [imported] - Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              504 RAPAGTLCLRTLVEHSGRVFRLQFDBPQIVSSSHDDTI 541
                                                                                                                         Ν̈́D
                                 A,Cross-references: SGD:SO001308; MIPS:YIL046w
A,Map position: 9L
C.Superfeamily: unassigned WD repeat proteins; F
F;298-329/Domain: WD repeat homology «WDD:
F;338-369/Domain: WD repeat homology «WD2>
F;374-409/Domain: WD repeat homology «WD2>
F;417-450/Domain: WD repeat homology «WD3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430 KRGIACLQYRD--RLVVSGSS.
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A:Introns: 75/3; 319/1; 354/1
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C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S:
Matches 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189
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                                                                                                                    GSPDB:GN00066; SPDB:SPAC57A10.05c
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Nylternate names: protein Y19905.02; protein Y10046w

Nylternate names: protein Y19905.02; protein Y10046w

Nylternate names: protein Y19905.02; protein Y10046w

Cypecies: Sacharomyces cerevisiae

Cypecies: Sa-May-1993 Heequence_revision 24-Feb-1995 #text_change 26-May-2000

Cypecies: Saloman, S.

Rydell, C.; Bowman, S.

Submitted to the EMBL Data Library, December 1994

RyReference number: 849931

RyReference number: 849931

RyReferences: 1-640 < ODE>

RyReferences: 1-640 < ODE>

RyResidus type: DNA

RyResidus type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          264 ---CRQVVLSGHSDGVMCLQLVRNILASGSXDATIRLWNLATFQQVALLEGHSSGVTCLQ 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 FDQCKLISGSMDKTIRIWNYRTSECISILHGHTDSVLCLTFDSTLLVSGSADCTVKLWHF 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 DYPISSNEETISSVKPPSPNSDSKFFLPFKTRPWKEVYAERCR----VECNWRHGR---- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315 YDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDM 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 ASPTDITLRRVLVGHRAAVNVVDF--DDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     433 IACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKI 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 SSM----HNELSGLSBKSRQRVEAVWAAFSEASCSERKLALQGILNNCSSSLLSFASSTL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDBFQIVSSSHDDTILIWDFLNDP 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 KPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 ------KPPDGNAPPNSF----YRALYPKIIQDIETIESNWRCGRHSLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIHCR----SETSKGVYCLQYDDQXIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 SSMIVPKORKLSASYEKEKELCVKYFEQWSE---SDQVEFVEHLISQMCHYQHGHINSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 INRK-----CEKCGWGLPLJERNTLYAAKASIQKRYERLTKRGVDQAHESSPVKKAKLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVWEACE-------CVHTLKNHSEPVTSVALGDCEVVSGSEDGKIYLWLFNNAP
                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 605;
                                                                                                                                                                                                                        %;Gene: SPDB:SPAC57A10.05c
%;Gene: SPDB:SPAC57A10.05c
%;Map position: 1
7;Superfamily: unassigned WD repeat proteins; WD repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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A. Accession: 843750
A. Residues: 1-60, 11, 62-640 (THO)
A. Cross-references: EMBL: L26505; NID: 9432493; PID: 9432494
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
19.5%; Score 590.5; DB 2;
Best Local Similarity 29.0%; Pred. No. 8.6e-38;
Matches 156; Conservative 86; Mismatches 189;
4;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                A;Cross-references: EMBL:294864; PIDN:CAB08168.1; G
A;Experimental source: strain 972h-; cosmid c57A10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 VRTDSLWRGLAERRGWGQYLFKN---
                                     A, Molecule type: DNA
A, Residues: 1-605 <BAD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                493
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hypothetical trp-asp repeat-containing protein - fission yeast (Schizosaccharomyces pomb CiSpecies: Schizosaccharomyces pombe CiSpecies: Schizosaccharomyces pomber 238502, Se62507
Schizosaccharomyces: Data Library, October 1995
A;Reference number: Z21798
A;Reference number: Z21798
A;Accession: T38502
                                            72 KTKLANGTSSMI------VPKQRK--LSASYEKEKEL-----CVKYFEQWSESDQVE 115
                                                                                                                                                                                116 FVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELV 175
                                                                                                                                                                                                                                                                                                                    227
                                                                                                                                                                                                                                                                                                                                                                                                                                                            273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 QIHDDVLVIGSDDNILKVWCIDKGEVMYTLVGHIGGVWISQISQCGRYIVSGSIDRIVKV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         392 AVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDR--LVVSGSSD 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 IGLIVTASSDRILRIWDITIGHCIRIIHAHQRGIACAQYNGKFIVSGSSDLTIRIFEASS 179
                                                                                                                                                                                                                                                                                                                                                                               143 SKNWKLISEIDKIWKSLGVEEFKHHPDPTDRVTGAWQGTAIAAG-----VTIPDHIQP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDLINVHRFLKLOKFGDIFERAADKSRYLRADKIEKNWNANPIMGSAV-LRGHEDHVITCM 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OYDDOKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLOYDE--RVIITGSSDSTVRV 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WDVNTGEMINTLIHHCEAVLHIRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09
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                                                                                                                                                                                                                                ESSYSNGSSSSYNADKLSSSRPLQHKLDLSASPSRNNDLNPRVEHLIALFKDLSSAEQMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450 NTIRLWDI---ECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 DNTIKIWDKNTLECKRILTGHTGSVLCLQYDER--VIITGSSDSTVRVWDVNTGEMLNTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 DRIVSVWDVNSRFILYKLYGHSGSVLCLDFCRRRNLLVSGSSDSTIIIWDWQNRRPLKVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FGHTDNVLGVVVSENYIISSSRDHTARVWRLDATSPAEACM-HVLRGHLASVNSVQYSSK
                                                                                                                                                                                                                                                                                                                    CKEWYRVTSDGMLWKKL-IERMV------RTDSLWRGLAERRGWGQYLFKNKPPDGNAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 PN-SFYRALYPKIIQDI-------ETIESNWRCGRHSLQRIHCREETSKGVYCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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17.1%; Score 519.5; DB 2; Length 26
Best Local Similarity 38.0%; Pred. No. 8.8e-33;
Matches 104; Conservative 58; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              507 AGTLCLRTLVEHSGRVFRLQ-FDEFQIVSSSHDDTILIWD 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          484 EGT-CVHMLSGHRSAITSLQWFGRNMVATSSDDGTVKLWD 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196
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                                                                                the
C;Function:
A;Description: negatively regulates sulfur structural gene expression
A;Note: scon-2+ expression is dependent on CYS3 function and the binding of CYS3 to
C;Superfamily: unassigned WD repeat proteins; WD repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                                                                                                                                                                                  11;
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A,Cross references: EMBL:Z79757, PIDN:CAB02129.1; GSPDB:GN00023; CESP:F55B12.3
A.Experimental source: clone F55B12
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                            LGGILSQLCFPQLSFVSREVNEALKIDFISALPV----ELAGKVLCYLDTVSLTKAAQVS 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGT 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKP------P 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 QGRVTELADSHDSQDRSVNQHGKRPAAEAEEEDPIKKRQCMAAAEASKAVTQPKTRSWKA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 NILECKRILIGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLR 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- PRSG 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 VY----RDRWQVSYNWKNSRYKLSVL---KGHENGVTCLQLDDNILATGSYDTTIKIWNI 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 ETEECIRTLVGHTAGIRALQFDDSKLISGSLDHTIKVWNWHTGECLSTFAAHTDSVISVH 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F55B12.3 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C.Accession: T22703
                                                                                                                                                                                                                                                                                                                117 VEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : | : | : | : | ORWRILADSDAVWVRMCEQHYNRK-----CTKCGWGLPLLERKKLRNYTRQRQLAKGGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 DGNA------PPNSFYRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDK
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.Introws: 22/3; 45/2; 77/3; 122/3; 171/2; 211/2; 342/2; 417/3; 478/3;
                                                                                                                                                                        Query Match 17.5%; Score 531.5; DB 2; Length 650; Best Local Similarity 25.0%; Pred. No. 3.6e-33; Matches 144; Conservative 76; Mismatches 180; Indels 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70;
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17.1%; Score 520; DB 2; Length 579
Best Local Similarity 28.8%; Pred. No. 2.4e-32;
Matches 150; Conservative 78; Mismatches 222; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STMRLWDSATGRCLRTLFGHLEGVWSLAGDTIRVISGANDGMVKTWE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          510 LCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDF 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, September 1996 A;Reference number: Z19602 A;Accession: T22703 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-579 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Gene: CESP: F55812.3
A, Map position: 5
A, Introws: 22/3; 45/2:
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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-75 < XCM> A;Cross-references: EMBL;Y08391; PIDN:CAA69671.1 A;Experimental source: strain h- 972 R;Mood, V.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M. S;Mood, V.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M. S;Mood, V.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M. S;Mood, V.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M. A;Reference number: 221842 A;Accession: T40157 A;Accession: T40157 A;Accession: T40157 A;Accession: T40157 A;Molecule type: DNA A;Residues: 1-775 < WOO> A;Coss-references: EMBL;AL022103; PIDN:CAA17898.1; GSPDB:GN00067; SPDB:SPBC2G2.18 A;Reperimental source: strain 972h-; cosmid c2G2 C;Genetics: C;Genetics: A;Mop Desition: 2 A;Note: pop1+	Query Match       14.9%; Score 453; DB 2; Length 775;         Best Local Similarity 25.8%; Pred; No. 5.8e-27;         Matches 162; Conservative 86; Mismatches 229; Indels 150; Gaps 20;         QY       9 QEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTY-NSCARLCLNQET 56         :                     :                   Db       121 REKCLKRRNSSLSSNLHANKRFLFNSQSDGNKKNETFPSTNYSNVFYPNNCDSKEVASET 180         QY       57 VC	DD 181 TFSLDAPNNSVNYSYFSPNLLGNDSKTRQSFPPHSSSSHNSLHEPVIXDFSENPSIHP 240  QY 93SYEKEKELCVKYFEQMSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDF 144  DD 241 SNHLSSQKNAVLKLAQLISSFEKLPESVRQYLLFHLLSRCGKHAVQNIHKILLPIFGKNF 300	Qy 145 ITALPARGLDHIAENILSYLDAKELCAAELVCKENYR-VTSDGMLWKKL1 193	SLSAETSKGVYCLETSKGVYCITKL	450 WTFBYVGDTLVTGSTDRTVRVWDLRTGECKQVFYGHTSTIRCIKIVQGNQS 371 VWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWN 371 VWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWN 506DVEKENRPASNDANSMPPYIISSSRDCTIRLWSLPCLD 417TSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIR	Db 553 NPDQNNDFTSATTNPFYIRTLRGHTDSVREVACLGDLIVSASYDGTLEVWKASTGVC 609  Qy 463 LRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSG 520	Qy 521 RVFRLQFDEFQIVSSSHDDTILIWD 545	RESULT 11 AEIBL 1 AEIBL 1 MD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
DPRAPAGILCLRILVEH- 518	A; Ittle: A gene responsible for vegetative incompatibility in the rungus Podospora anser A; Reference number: 218944; MUID:9609891; PMID:7557402 A; Accession: T18521 A; Accession: T18521 A; Accession: Preliminary; translated from GB/EMBL/DDBJ A; Residue: preliminary; translated from GB/EMBL/DDBJ A; Residue: 1-1356 < SAU> A; Cross-references: EMBL:L28125; NID:g607002; PID:g607003; PIDN:AAA85775.1 A; Genetics: A; Chartons: 761/3	<pre>Query Match Best Local Similarity 31.7%; Pred. No. 8.2e-27; Matches 121; Conservative 64; Mismatches 131; Indels 66; Gaps 15;  Qy 226 APPNSFYRALYPKIIQDIETIESNWRGGRHSL</pre>	Db 802 APTDSMIKKIFKKEEPGMISTISVVEAEWNACTQTLEGHGSSVLSVAFSADGRVASGSD 861  Qy 265ETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRIL 303  Db 862 DKTIKIWDTASGTGTQTLEGHGGSVWSVAFSPDRERVASGSDDKTIKIWDAASGTCTQTL 921	QY 304 TGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFN-NGMM 360  bb 922 EGHGGRVQSVAFSPDGQRVASGSDDHTIKIWDAASGTCTQTLEGHGSSVLSSVAFSPDGQR 981  QY 361 VAC-SKDRSIAWDWASFTDITLERNUNGPDEXIVOSASGDRTIKWWNT 417  Db 982 VASGSGDKTIKIWDTASGTCTQTLEGHGGSVWSVAFSPDGQRVASGSDDKTIKIWDT 1038	QY 418 STCEPVRILNGHKRGIACLQYRDRLUVSGSSDNTIRLWDIECGACLRVLEGHEELVRC 475	Qy 532 IVSSSHDDTILIWDFANDRAQ 553  DD 1150 VASGSIDGTIKIWDAASGTCTQ 1171	RESULT 10 T4136   WD repeat protein popl [imported] - fission yeast (Schizosaccharomyces pombe) C.Species: Schizosaccharomyces pombe C.Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000   C.Accession: T45136; T40157	R;Kominami, K.; Toda, T. subrary, September 1996 submitted to the EMBL Data Library, September 1996 A;Description: Fission yeast WD repeat protein Popl is involved in maintenance of ploidy A;Reference number: 222925 A;Accession: T45136

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A;Reference number: S48310
A;Reference number: S48310
A;Reference number: S48310
A;Residues: 1-579 < CHU>
A;References: EMBL: Z46255; NID: G559925; PIDN: CAA86341.1; PID: G559926; MIPS: YFL009w
R;YOchem, J; Byers: B
J. Mol. Biol. 195, 233-245, 1987
A;Rile: Structural comparison of the yeast cell division cycle gene CDC4 and a related : A;Reference number: A26867; MUID: 88011240; PMID: 3309335
A;Accession: A2687
A;Accession: A2687
A;Accession: A2687
A;Accession: BMBL: X05625; NID: G3502; PIDN: CAA29113.1; PID: G3503
A;Reference number: 862302
A;Reference number: 862302
A;Accession: S62304
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A;Residues: 1-779 <MUW>
A;Cross-references: EMBL:D31600; NID:g836814; PIDN:BAA06495.1; PID:d1007066; PID:g836815
C;Genetics:
                                                         PIDN:BAA09229.1; FID:d1009870; PID:g836745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HWASVRTVSCHGNIVVSGSYDNTLIVWDVAQMKCLYILSCHTDRIYSTIYDHERKKCISA 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          226 APPNSFYRALYPKIIQD-----IBT--IESNWRCGRHSLQRIHCRSETSKGVYCLQYD 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSLNLKLSQKYPKLSQQDRLRLSFLENIFILKNWYNPKFVPQRTTLRGHMTSVITCLQFE 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOKIVSGLRDNTIKIMDKNTLECKRILIGHTGSVLCLQYDE-RVIITGSSDSTVRVWDVN 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNYVITGADDKMIRVYDSINKKFLLQLSGHDGGVWALKYAHGGILVSGSTDRTVRVWDIK 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 TGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASFTDITLRRVLVGHRAAVNV 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----HVFKGHNSTVRC 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 SESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LCAAELVCKEWYR-VTSDGMLWKKLI--ERMVRTDSLWRGLAERRGWGQYLFKNKPPDGN 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SPKGF 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 TVCLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEK-----ELCVKYFEQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 TIPLAKTIKTINN -----NNNIADLIESKOSIISPEYLSDEIFSAINNNIPHAYFK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Gene: SGD:CDC4
A,Cross-references: SGD:S0001885; MIPS:YFL009w
A,Map position: 6L
C,Function: A,Description: initiation of DNA replication; separation of the :
C,Superfamily: unassigned WD repeat proteins; WD repeat homology C,Keywords: cell cycle control
F,459-494/Domain: WD repeat homology <WD1>F;628-659/Domain: WD repeat homology <WD2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.2%; Score 399; DB 2; Length 779; Best Local Similarity 24.3%; Pred. No. 9.1e-23; Matches 139; Conservative 80; Mismatches 196; Indels 1
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A;Molecule type: DNA
A;Residues: 1-779 <MUR>
A;Cross-references: EMBL:D50617; NID:g836685;
R;Churcher, C.
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N;Alternate names: protein YFL009w
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 02-Sep-1995 #sequence revision 12-Apr-1996 #text_change 26-May-2000
C;Accession: S56245; S48310; A26867; S62304
R;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu submitted to the BMBL Data Library, May 1995
A;Reference number: S56186
                      C)Accession: AE1810
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, G DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; WUID:21595285; PMID:11759840
A;Accession: Ab1810
A;Acceus: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                           A,Residues: 1-1227 <KUR>
A,Cross-references: GB:BA000019; PIDN:BAB77553.1; FID:g17135007; GSPDB:GN00179
A,Experimental source: strain PCC 7120
C,Genetics:
A,Gene: alr0029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 IIQDIETIESN------WRCGRHSL---QRIHCRS-----ETSKGVYCLQY--D 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 DOKIVSGLRDNTIKIWDKNTLECKRILIGHTGSVLCLQY--DERVIITGSSDSTVRVWDV 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKYFATGLMNGEIRLWQTSDNKQLRIYKGHTAWVWAFRAFSPDSRMLASGSADSTIKLWDV 673
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
13.6%; Score 413.5; DB 2;
Best Local Similarity 23.9%; Pred. No. 1.3e-23;
Matches 140; Conservative 114; Mismatches 209;
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A;Reference number:
A;Accession: S56245
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Qy 260	Db 361 KDRIITTSGSGTIOIHNAITGVLEARLEGHKEGVWAVKHENTUSSGSIDKTVRVWNIEK 420  Qy 297 LECKRILTGHTGSVLCLQY	Qy 341 NTLIHHCEAVLHLRENNGMYVTCSKDRSIAVWDWASPTDITLRRVLVGHRAAVNVUDEDD 400  Db 473KLFKNTDPPYLPDNTNSIDRWE-KNPYFVHTLIGHTDSYRTISGYG 517  Qy 401 KYIVSASGDRIIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIE 458  :	Qy 459 CGACLRVLEGHEELVRCIRFDNKRINSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEH 518	RESULT 14 A12493 WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha C;Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002	C;Accession: A12493 R;Karako, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi R;Karako, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. B, 205-213, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUD:21595285; PMID:11759840 A;Recession: A12493 A;Status: preliminary A;Nolecule type: DNA A;Residues: 1-1189 <kur> A;Residues: 1-1189 <kur> A;Cross-references: GB:BA000020; PIDN:BAB76213.1; PID:g17135667; GSPDB:GN00180 A;Experimental source: strain PCC 7120 C;Genetics: A;Gene: a1r7129 A;Gene: a1r7129</kur></kur>	Query Match 12.5%; Score 378.5; DB 2; Length 1189; Best Local Similarity 26.7%; Pred. No. 6.4e-21; Matches 96; Conservative 63; Mismatches 107; Indels 93; Gaps 10; Qy 280 IVSGLEDNITHEWENTLECKRILIFGSVECLOONERVITIGSSBSTVRVWDVTG 337	Db 745 LASGSFDQNTHING HIGH HIGH HIGH HIGH HIGH HIGH HIGH	Qy 357NGMAVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVMVVDFDDKYIVS 405    S	Qy 464 RVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDP 503
	DS 539 SMD11IKIWDLENIWNNGECSIAIRSASPCANIIGGAMTILGGHIALVGLLKLSDKFLVSA 648  27 536 SHDDTILIWDFLNDPAQABPPRSPSRTYTY 566  549 AADGSIRGWD-ANDYSRKFSY 668	RESULT 13 143557 F-box/WD-repeat protein pop2 - fission yeast (Schizosaccharomyces pombe) N.Alternate names: protein pop2 - factor sudip C.Species: Schizosaccharomyces pombe C.Species: Schizosaccharomyces pombe C.Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000 C.Accession: 143577; 173799 R.Molf D A .Jackson D K.	Submitted to the EMBL Data Library, December 1997 A; Description: Fission yeast pop2 encodes a novel F-box/WD-repeat protein involved in the A; Reference number: 222576 A; Accession: 143557 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Readlous: preliminary; translated from GB/EMBL/DDBJ A; Readlous: 1-703 < WQLD A; Readlous: 1-703 < WQLD A; Cross-references: EMBL, RP08667; PIDN: AAB95480.1	Ricenties, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, August 1996 A.Reference number: Z21812 A.Accession: T38794 A.Status: preliminary; translated from GB/EMBL/DDBJ	A; Residues: 1-703 cGEN- A; Cross-references: Enrain 9721-; cosmid c4D7 A; Cross-references: Enrain 9721-; cosmid c4D7 A; Experimental source: strain 9721-; cosmid c4D7 A; Ballepalli, P.V.; Tien, D.; Kelly, T.J. Proc. Natl. Acad. Sci. Uc.S., 95, 8159-8164, 1998 A; Title: Sudl+ targets cyclin-dependent kinase-phosphorylated Cdc18 and Ruml proteins fd A; Reference number: 222686; MUD: 98318628; PMID: 9653157 A; Accession: T43798 A; Accession: T43798 A; Accession: T43798 A; Residues: 1-703 cJAL> A; Residues: DPI: ACCESSION: A; Residues: EmbL: AF064515; NID: 93293382; PIDN: AAC39496.1; PID: 93293383 A; Gene: pop2: sudl; SPAC4D7.03 A; Gene: Lice A; Combaction: 1 C; Function:	A; Description: required to prevent spontaneous re-replication Query Match Best Local Similarity 23.3%; Pred. No. 1.2e-22; Matches 146; Conservative 92; Mismatches 226; Indels 163; Gaps 25;	QY 14 KFMNSSEREDCNNGEPPRKIIPEKNSLROTYNSCARLCLNQETVCL 59	Db   155 NSISSNSDNFPPSPKVDISNTVSPGSKPISEDLEDLNLGSIVQTFEDLPEGIQ-SYAF 211   Qy   119 HLISQNCHYQHGH-INSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCK 177   Db   212 FQLLRSCNRQSMRLLLNBCEPLLKKDILSNLPFSIVQSILLNLDHISFLSCRLVSP 267   Qy   178 EWYRVTSDGMLWKKLIERNVRTDSLWRGLAERRGWGOYLFYKKPPDGNAPPN 229	DD 268 TWNRILDVHTSYWKHMFSLEGFQINENDWKYANPUNRPFELHND 312  QY 230 SFYRALYPKIIQDIETIESNWRCGRHSLQR

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R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change_09-Dec-2002
C;Accession: AC1842
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1747 < KUR>
A;Cross-references: GB:BA000019; PIDN:BAB77807.1; PID:g17135261; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: allo283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276 DDQKIVSGLRDNTIKIWDKNTLECKRILIGHTGSVLCLQY--DERVIITGSSDSTVRVWD 333
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1045 NQYLATGGDDSVVRLWDIGKGVCVRTFSGHTSQVICILFTKDGRRMISSSSDRTIKIWN 1103
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Harper J.W.;
"The SCF(beta-TRCP)-ubiquitin ligase complex associates specifically
with phosphorylated destruction motifs in I-kappa-B-alpha and
beta-catenin and stimulates I-kappa-B-alpha ubiquitination in vitro.";
Genes Dev.: 13;270-283(1999).
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MEDLINE SERVE SERVE S. P., Durand H., Selig L., Benichou S., Richard V., Margottin F., Bour S.P., Durand H., Benarous R.;
"A novel human MD protein, h-beta TrCp, that interacts with HIV-1 Vpu connects CD4 to the ER degradation pathway through an F-box motif.";

Modus Cell 1555 574 41998 A.
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69Y297; 09Y213;

6-0CT-2001 (Rel. 40, Last sequence update)

16-0CT-2001 (Rel. 40, Last annotation update)

15-SEP-2003 (Rel. 42, Last annotation update)

16-SEP-2003 (Rel. 40, Last sequence update)

17-SEP-2003 (Rel. 40, Last sequence update)

18-SEP-2003 (Rel. 40, Last annotation update)
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MEDLINE=99075339, PubMed=9859996,
Maron A., Hatzubai A., Davis M., Lavon I., Amit S.,
Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
"Identification of the receptor component of the Ikappabalpha-
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
Q15542
Q9epv5
Q9epv5
Q8 B3 G
Q8 B3 G
Q14727
Q24456
P3 B129
P16649
P6699
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MEDLINE-20003060; PubMed=10531035;
Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W.,
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                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
     APAP RAT
APAP RAT
YKL6 YEAST
YUL1 SCHPO
APAF MOUSE
GBLP BRANA
APAF HUWAN
APAF HUWAN
T224 YEAST
TUP1 YEAST
TUP2 KKUUSA
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MEDLINE-99145464; PubMed-9990852;
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TRCB XENLA
FWIB HUMAN
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POFB SCHPO
POFI SCHPO
SCOB EMENI
MT30 YEAST
SCO2 NEUCR
SE10 CAEEL
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Maximum Match 100%
Listing first 45 summaries
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us-09-601-168b-2.rsp

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421 VLVGHRAANNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVV 480
                     PKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDF 180
                                                                                                                                                                                        ETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGS 324
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MATURED COCYTES, THE LEVEL CHANGE VERY LITTLE EVEN AFTER ZYGOTIC
GENE TRANSCRIPTION BEGINS FOLLOWING THE MIDBLASTULA TRANSITION. DO
                                                                                                                                                                                                                        ETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGS
                                                                                                                                                                                                                                                                              SDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRR
                                                                           ITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWR
                                                                                                                       GLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRS
                                                                                                                                              241 GLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRS
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   (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=93330289; PubMed=8393141;
MEDLINE=93330289; PubMed=8393141;
MEDLINE=93330289; Stratowa C., Castanon M.J.;
Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in anaphase are rescued by Xenopus cDNAs encoding N-ras or a protein with beta-transducin repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: Probably recognizes and binds to some phosphorylated proteins and promotes their ubiquitination and degradation. May
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hudson J.W., Alarcon V.B., Elinson R.P.; "Identification of new localized RNAs in the Xenopus occyte by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRCB_XENLA STANDARD; PRT; 518 AA.
091854; P70037; P70038;
15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Beta-TrcP (Beta-transducin repeat-containing protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            participate in Wnt signaling.
SUBUNIT: PART OF A SCF (SKP1-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97109804; PubMed=8952061;
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Dev. Genet. 19:190-198(1996)
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box protein) ubiquitin ligase complex, which mediates the ubiquitination of proteins involved in cell cycle progression, signal transduction and transcription. Regulates the stability CTNNB1 and participates in Wnt signaling.
                                                                  PATHWAY: Ubiquitin conjugation, third step.
SUBMUT: Interacts directly with SKP1 in the SCF complex.
Interacts specifically with phosphorylated CINNB1 and NFKBIA, ubiquitination substrates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIN, 603482; -.
GO; GO:0004840; F:ubiquitin conjugating enzyme activity; TAS.
GO; GO:0007165; P:signal transduction; TAS.
GO:0006511; P:ubiquitin-dependent protein catabolism; TAS.
InterPro; IPR001810; F-box.
InterPro; IPR001881; Wu340.
Pfam; PF00646; F-box; 1.
Pfam; PF00646; F-box; 1.
Prom; PR00180; Wq90.
Propom; PR00180; Wq90; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.1%; Score 3006; DB 1; Length 605; 94.0%; Pred. No. 8.6e-220; ive 0; Mismatches 0; Indels 3
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WD 2.
WD 4.
WD 5.
WD 6.
WD 7.
Missing (in isoform 2).
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                                                                                                                                                                         Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                        IsoId=Q9Y297-1; Sequence=Displayed;
                                                                                                                                                                                                                                      IsoId=Q9Y297-2; Sequence=VSP 00676.
SIMILARITY: Contains 1 F-box domain.
SIMILARITY: Contains 7 WD repeats.
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                                                                                                                                     SUBČELLULAR LOCATION: Cytoplasmic. ALTERNATIVE PRODUCTS:
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les 569; Conservative
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SMART; SM00320; WD40; 7.
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343 TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVMNTSTCEFVRTLNGHKRGIACLQ 402
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Stotani H., Nomura N., Ohara O.;
Stotani H., Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. X.
The complete sequences of 100 new cDNA clones from brain which can
code for large proteins in vitro.";
DNA Res. 5:169-176[1998].
-- FUNCTION: Probably recognizes and binds to some phosphorylated
proteins and promotes their ubiquitination and degradation. May
participate in Wnt signaling.
-- SUBUNIT: PART OF A SCF (SKPI-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX.
-- SUBURIT: PART OF A SCF (SKPI-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX.
-- SUBCRELIVIAR LOCATION: Cytoplasmic (Potential).
                                                                        YRDRLVVSGSSDNTIRLWDI ECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL
                                                                                                                                                                                                                                                                                                     Q9UKEI; Q9P2S8; Q9P2S9; Q9Y4C6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
F-box/WD-repeat protein 1B (F-box and WD-repeats protein beta-TrCP2)
FEXWIB OR FBWIB OR BTRCP2 OR KIAA0696.
                                                                                                                                                  Σ.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Koike J., Sagara N., Kirikoshi H., Takagi A., Miwa T., Hirai M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning and genomic structure of the betaTRCP2 gene chromosome 5q35.1.";
Biochem. Biophys. Res. Commun. 269:103-109(2000).
                                                                                                                                VAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of a family of human F-box proteins."; Curr. Biol. 9:1177-1179(1999).
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                                                                                                                                                                                                                                                                                   542 AA
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IsoId=Q9UKB1-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                     PRT;
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MEDLINE=20160458; PubMed=10694485;
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MEDLINE=98403880; PubMed=9734811;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=B
                                                                                                                                                                                                                                                                                     HUMAN
                                                                                                                                498
                                            438
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                                                                                                                                                                                                                                                                FW1B_HUMAN
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                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FWBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRIIKVWNTSTCEFVRTLNGHKRGIACLQ 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 GTSSMIVPKQRKLSANYEKEKELCVKYFEQWSECDQVEFVEHLISRMCHYQHGHINTYLK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASP 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVIIIGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 GISSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 PMLQRDFITALPARGLDHIAENILSYLDAKSLCSAELVCKEWYRVTSDGMLWKKLIERMV 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 SSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLAN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QRIHCRSEISKGVYCLQYDDQKIVSGLRDNIIKIWDKNTLECKRVLMGHTGSVLCLQYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 ASEREDCNRDEPPRKIITEKNIDRQ-----TKLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIDSLWRGLABRRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIDSIMRGLABRRGWGQYLFKNKPPDGKIPPNSFYRALYPKIIQDIETIESNWRCGRHSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
  Q.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        signaling pathway, Repeat, WD repeat. F-BOX.
    INCREASE IN ABUNDANCE IN THE GASTRULA, NEURULA, TAILBUD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2597; DB 1; Length 518;
Pred. No. 6e-189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MD 1.

WD 2.

WD 3.

WD 4.

WD 5.

WD 6.

WD 7.

GEM -> BER (IN REF. 2).

GLA -> AAH (IN REF. 2).
                                         SIMILARITY: Contains 1 F-box domain.
SIMILARITY: Contains 7 WD repeats.
SIMILARITY: STRONG, TO C.ELEGANS K10B2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 85.6%; Score 2597; D il Similarity 91.6%; Pred. No. 6e-1488; Conservative 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50161; FBOX; 1.
PROSITE; PS50678; WD REPEATS 1; 6.
PROSITE; PS50808; WD REPEATS 2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59507 MW;
                                                                                                                                                                                                                                                                                                                               EMBL; U63921; AAB49671.1; -.
BMBL; U63922; AAB49672.1; -.
PIR; B4808; B4808.
InterPro; IPR001810; F-box.
InterPro; IPR00180; W440.
Pfam; PF00646; F-box; 1.
PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jbl conjugation pathway; Wnt
JOMAIN 119 157
                                                                                                                                                                                                                                                                                                            EMBL; M98268; AAA02810.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302
302
516
518 AA;
                         TADPOLE EMBRYO
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Best Local 8
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REPEAT
REPEAT
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Matches
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EMBL; U28730; AAA68258.2; -..
WormPep; K10B2.1; CE28600.
GO; GO:0005737; C:cytoplasm; NAS.
GO; GO:0008285; P:negalive regulation of cell proliferation; IMP.
InterPro; IPR001810; F-box.
InterPro; IPR001680; W040.
                                                                                                                                                                                 Lig3 CAEEL STANDARD; PRT; 665 AA. 005990, Ogdruns; Created) 15-JUL-1998 (Rel. 36, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) F-box/WD-repeat protein lin-23. OR KIOB2.1.
                                                                                                        DILIMDFLNVPPSAQNETRSPSRTYTYISR 542
                                                                                          DTILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Contains 1 F-box domain. SIMILARITY: Contains 7 WD repeats. SIMILARITY: STRONG, TO X.LAEVIS FBXW1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF275253; AAG28037.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam, PF00646, F-box; 1.
Pfam, PF00400; WD40; 7.
                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                               NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     levels.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 HLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 HLISRMCHYOHGHINSYLKPMLORDFITALPEGGLDHIAENILSYLDARSLCAAELVCKE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CKRILIGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNG 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 LMVTCSKDRSIAVWDWASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWSTS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419 TÇEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 WQRVISEGMLWKKLIERMYRTDPLWKGLSERRGWDQYLFKNRPTDG--PPNSFYRSLYPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLKVLIGHTGSVLCLQYDERVIVTGSSDSTVRVMDVNTGEVLNTLIHHNEAVLHLRPSNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MDPABAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 S--TAMKTENCVAKTKLANGTSSMIVPRQRKLSASYEKEKELCVKYFEQWSESDQVEFVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 WYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 IIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 IIQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISGLRDNSIKIWDKTSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                   PROSITE; PSS0181; FBOX; 1.

PROSITE; PSS0181; FBOX; 1.

PROSITE; PSS0082; WD_REPEATS_1; 5.

PROSITE; PSS0082; WD_REPEATS_2; 7.

PROSITE; PSS0084; WD_REPEATS_2; 7.

UD1 conjugation pathway; Wnt signaling pathway; Repeat; WD repeat;

Alternative splicing.

DOMAIN 129 167 WD 1.

REPEAT 278 315 WD 1.

REPEAT 278 315 WD 2.

REPEAT 318 355 WD 3.

REPEAT 401 440 WD 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                          /FIId=VSP 006765.
CSVPRSIMLGCANLVESMCALSCLQSMPSVRCL
MEDQNEDESPKKNTLM (in isoform B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 78.6%; Score 2384.5; DB 1; Length 542; Best Local Similarity 79.0%; Pred. No. 7.6e-173; Matches 451; Conservative 48; Mismatches 41; Indels 31;
                                                                                                    GO, GO:000151; C:ubiquitin ligase complex, NAS.
GO; GO:0004842; F:ubiquitin ligase activity; NAS.
GO; GO:0016867; P:ubiquitin-protein ligase activity; NAS.
INTERPRO; IPROUBLO; P:procein ubiquitination; NAS.
INTERPRO; IPROUBLO; F-box.
InterPro; IPROUBLO; F-box; I.
PRINTS; PROOBO; WD40; 7.
PRINTS; PROOBO; WD40; 7.
SWART; SMOOBS6; FBOX; 1.
SWART; SMOOBS6; FBOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7CD40087EFAA5C8A CRC64;
           EMBL; AF176022; AAF04528.1; --
EMBL; AB03329; BAA42329.1; --
EMBL; AB033280; BAA92330.1; --
EMBL; AB033281; BAA92331.1; --
EMBL; AB044596; BAA92331.1; --
Genew; HGNC:13607; FEXWIB.
                                                                                                                                                                                                                                                                                                                                       WD 1.
WD 2.
WD 4.
WD 5.
WD 6.
WD 7.
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392 TCEFVRTLWGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF 451
                                                                                                                                     DNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHD
                                                                                                                                                                                         Submitted (AUG-2001) to the EMBL/GenBank/DDBU databases.
Submitted (AUG-2001) to the EMBL/GenBank/DDBU databases.

-!- FUNCTION: Functions cell autonomously to negatively regulate cell cycle progression. Required to restrain cell proliferation in response to developmental cues. Probably recognizes and binds to some proteins and promotes their ubiquitination and degradation (By similarity).

-!- GUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (By similarity).
SOBCELLURAR LOCATION: Cytoplasmic (Potential).
DEVELOPMENTAR STAGE: Highest levels in embryos and adults, lowest levels in larvae. Maternal expression results in high zygotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., FUNCTION, DEVELOPMENTAL STACE, AND MUTAGENESIS. MEDLINE=20515608; Pubmed=11060233; Kipreos E.T., Gobel S.P., Hedgecock E.M.; The Caenorhabditis elegans F-box/WD-repeat protein lin-23 functions to limit cell division during development."; Development 127:5071-5082(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A.
STRAIN=Bristol N2;
Miller N.:
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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NCBI_TaxID=4896
                                     SEQUENCE
88 RKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITA 147
                                                                                                                                                                                                                               247
                                                                                                                                                                                                                                                            GSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDR 367
                                                                                                                                                                                                                                                                                                                                                                      GHKRGIACLOYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGA 487
                                                                                                                                                                                                                                                                                                                                                                                443 YDGKIKVWDLQAALDPRALSSEICLCSLVQHTGRVFRLQFDDFQIVSSSHDDTILIWDFL 502
                                                                                                                                                                                                                       LPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLA 207
                                                                                                                                                                                                                                                                                SNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILLTGHT 307
                                                                                                                                                                                                                                                                                                                                          SIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLN 427
                                                                                                                                                                                                                                                                                                                                                      323 SIAVWDMVSPRDITIRRVLVGHRAAVNVVDFDDRYIVSASGDRIIKVWSMDTLBFVRTLA 382
                                                                                                                                                                                                                                                                                                                                                                                                  488 YDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFL 547
                                                                                                                                                                                                        98
                                                                                                                                                                                                    263 GSVLCLQYDNRVIISGSSDATVRVWDVETGECIKTLIHHCEAVLHLRFANGIMVTCSKDR
                                                                                                                                                                                                                                                   -----FKNKPPDGNAPPNSFYRALYPKIQDIETIE
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                             29;
                                                                                                                                                              Length 665;
                                                                                                                                                                             92; Indels
                                                                                                                                ALA-RICH.
G->R: IN LIN-32(RH293).
BF3E9AF51F12ECCC CRC64;
                          DB 1;
                                                                                                                                                            54.0%; Score 1638.5; DB 1; 63.7%; Pred. No. 2.6e-116; live 59; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POFE SCHPO STANDARD; PRT; 506 AA. 00985; Q9P7V1; 01-FEB-1996 (Rel. 33, Created) 16-CCT-2001 (Rel. 40, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F-box/WD-repeat protein pof11.
POF11 OR SPAC29E6.01 OR SPAC30.05.
Schizosaccharomyces pombe (Fission yeast).
PRINTS; PR00320; GPROTEINBRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                             503 DAP----PSGLPSST 513
                                                                                                                                                75916 MW;
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      ProDom; PD000018; WD40; 4.
SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
                                                                                                                                                                           Matches 316; Conservative
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665 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 SGSSDSTIIIWDWQNRRPLKVYFGHTDNVLGVVVSENYIISSSRDHTARVWRLDATSPAE 337
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"Fission yeast F-box protein Pof3 is required for genome integrity and
relomere function ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RATLDSVYCVQYDDEIMVSGSKDRTVSVWDVNSRFILLYKLYGHSGSVLCLDFCRRRLLLV
                                                                                                                                                                                                                                                                                     67 ENCVAK----TKLANGTSSMIVPKORKLSASYEKEKELCVKYFEQWSESDQVEFVEHLIS
                                                                                                                                                                                                                                                                                                                                                                               123 QMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 QYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 -ETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDER--VII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                380 ITLRRVLVGHRAAVNVVDFDDK--YIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLO
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                                                                                                                                                                                                                                     Conservative 104; Mismatches 167; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 TSDGMLWKKLI-----ERMVRTDSLWRG------LABRRGWG-
                                                                                                                                                                                           22.7%; Score 690; DB 1; Length 506; 30.4%; Pred. No. 1e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 34), Last annotation update)
28-FEB-2003 (Rel. 34), Last annotation update)
28-FEB-2003 (Rel. 36, Last annotation u
                                                                                                                                              CEF34D4EFFBC2E10 CRC64;
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    telomere function.";
Mol. Biol. Cell 13:211-224(2002)
298 WD
338 WD
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426 WD
505 WD
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NCBL_TaxID=4896;
  259
301
345
388
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506 AA;
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nes 163; Conserv
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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              NEDLINE-21848101; PubMed=11859360;

Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., RaDLINE-21848101; PubMed=11859360;

Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Bourons J., Pears N., Chillingworth T., Churcher C.M., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Collins M., Connor R., Harris D., Hiddled T., Fraser A., Amoney B., Money B., Monles J., Hoursby T., Howarth S., Murbhy L., Niblett D., Odell C., James K., Jones M., Leather S., McDonald S., McLean J., Annering S., McLean J., Niblett D., Odell C., Almorat M., Parten D., Quail M.A., Rabbinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Richert B., Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woldward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Multibert H., Abrithardt R., Pohl T.M., Borzym K., Lenger I., Wambutt R., Purnelle S., McLiens M., Wedler H., Wambutt R., Purnelle S., M., Galieu E., Dreano S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang S., Hunt C., Moore K., Hurst S.M., Daga R.R., Cruzado L., Jimenez J., Sanchez M., Gelsel Rey F., Benito J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; Shraktong S.L., The Sender M., Rochen W., Pollace D., Ambirong Sequence Sequence of Schlzosaccharomyces pombe.";

Ruther 415: R71-88012002, Schlzosaccharomyces pombe.";

Ruther 415: R71-88012002, Schlzosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: Probably recognizes and binds to some phosphorylated proteins and promotes their ubiquitination and degradation.
-!- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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PRINTS; PROGAZO; GPROTEINBRPT.
PRODOM, PDOCOOL8; WA40; 3.
SWART; SW00320; WD40; 7.
PROSITE; PS50181; PBOX; 1.
PROSITE; PS5008181; PBOX; 1.
PROSITE; PS500818, WD_REPEATS_1; 2.
PROSITE; PS50081, WD_REPEATS_1; 2.
PROSITE; PS50084; WD_REPEATS_1; 2.
UDL conjugation; Repeat; WD_REPEATS_1 1.
101 CONJUGATION; Repeat; WD_REPEATS_1 1.
102 DOMAIN 107 153
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-!- SIMILARITY: Contains 1 F-box domain.
-!- SIMILARITY: Contains 7 WD repeats.
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EMBL; 224864; CAB08168.1; -.
PIR; T38932; T38932.
GeneDB SPombe; SPAC57A10.05c; -.
InterPro; IPR001810; F-box.
InterPro; IPR001810; WD40.
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Pfam; PF00400; WD40; 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        264 ---CRQVVLSGHSDGVMCLQLVRNILASGSYDATIRLWNLATFQQVALLEGHSGVTCLQ 320
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                                                                                                                                                                  102 DSLVRLDFLSLLPV----EISFRILSFLDARSLCQAAQVSKHWKELADDDVIWHRMCEQH 157
                                                                                                                                                                                                                                                                                                                                                          220 ------KPPDGNAPPNSF-----YRALYPKIIQDIETIESNWRCGRHSLQ 258
                                                                                                                                                                                                                                                                                                                                                                                                212 DYPTSSNEETISSVKPPSPNSDSKFFLPFKTRPWKEVYAERCR----VECNWRHGR---- 263
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                       SSMIVPKORKLSASYEKEKELCVKYFEQWSE---SDQVEFVEHLISQMCHYQHGHINSYL 136
                                                                       46 SSM----HNELSGLSEKSRQRVEAVWAAFSEASCSERKLALQGILNNCSSSLLSFASSTL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               543
                                                                                                                                                                                                                                                                                                 158 INRK-----CEKCGWGLPLLERNTLYAAKASIQKRYERLTKRGVDQAHESSPVKKAKLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPRESSION.
--- SIMILARITY: Contains 8 WD repeats.
--- SIMILARITY: Contains 1 F-box domain.
--- SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY OF WD-REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              493 KUWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Natorff R.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: REGULATORY PROTEIN THAT CONTROL SULFUR METABOLITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes,
Eurotiales, Trichocomaceae, Emericella.
NCBI_TaxID=162425;
                                                                                                                                                                                                                                         197 VRTDSLWRGLAERRGWGQYLFKN---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCOB_EMENI STANDARD; PRT; 678 AA. 000659; 15-JUL-1998 (Rel. 36, Created) 25-JUL-1998 (Rel. 36, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Sulfur metabolite repression control protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Emericella nidulans (Aspergillus nidulans)
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InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
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------RLVVSGSSDNTIRLWDIECGACLRVLEGHEEL 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 VEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 KNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376 TETGEBLRTLRGHESGIRCLQPDDTKLISGSMDRTIKVWNWRTGECISTYTGHRGGVIGL 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      612 VWALGADTLRIVSGAEDRMIKIWD-----PRIGKCERTFIGHSGPVTCIGLGDSRF 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVYKDRFKVGTNWKYGR-----CSIKTFKGHTNGVMCLQFEDNILATGSYDTTIKIWD 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              354 RFNNGMMYTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV--VDFDDKYIVSASGDRT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   492 VRLWDLDTKTCIRTFHGHVGQVQQVVPLPREFEFEFHDAECENDDLSTTSGDANPPSIQA 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIIQDIETIESNWRCGRHSLORIHCRSETSK----GVYCLOYDDOKIVSGLRDNTIKIWD
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WD 2.
WD 3.
WD 4.
WD 6.
WD 6.
WD 7.
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                         Pfam; PF00400; WD40; 7.
PRINTS; PR00320; GPRCTEINERFT.
ProDom; PD000016; WH40; 3.
SWART; SW00256; PB0X; 1.
R SWART; SW00256; WD40; 7.
R PROSITE; PS00181; FB0X; 1.
R PROSITE; PS00678; WD_REPEATS_1; 4.
R PROSITE; PS00678; WD_REPEATS_2; 7.
R PROSITE; PS00294; WD_REPEATS_2; 7.
R PROSITE; PS00294; WD_REPEATS_2; 7.
R PROSITE; PS00294; WD_REPEATS_ED00; 1.
R PROSITE; PS00294; WD_REPEATS_R PS00294; WD_REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.0%; Score 575; DB 1; 26.9%; Pred. No. 7.4e-36;
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(Rel. 31, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 640
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                                                                                                                                                                                                                                                                                                                                                                               224 F-
315 WD
415 WD
455 WD
456 WD
596 WD
597 WD
615 WD
615 WD
76070 MM
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663 ATGSEDCEVRMYSF 676
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Pfam; PF00646; F-box; 1.
Pfam; PF00400; WD40; 7.
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678 AA;
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01-FEB-1995
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MT30_YEAST
ID MT30_YEAST
AC P39014;
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Matches 149;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                           Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D.,
Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N.,
Harris D.E., Horsnell T., Hunt S., Jagels K., Jones M., Lye G.,
Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Rowley N.,
Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G.,
"The nucleotide sequence of Saccharomyces cerevisiae chromosome IX.";
Nature 387:84-87(1997).
-i. FUNCTION: NEGATIVELY REGULATES SULFUR AMINO ACIDS BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBUNIT: SEEMS TO INTERACT WITH MET4.
-!- SIMILARITY: CONTAINS 1 F-box domain.
-!- SIMILARITY: CONTAINS 8 WD repeats.
-!- SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY OF WD-REPEAT.
                                                                                                                                                                                                                                                      "Met30p, a yeast transcriptional inhibitor that responds to S-adenosylmethionine, is an essential protein with WD40 repeats."; Mol. Cell. Biol. 15:6526-6534(1995).
                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                         MEDLINE=96069360; PubMed=8524217;
Thomas D., Kuras L., Barbey R., Cherest H., Blaiseau P.L.,
Surdin-Kerjan Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> I (IN REF. 1).
5135D4BCA2E1EB97 CRC64;
                                                                                                Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WD 1.
WD 2.
WD 4.
WD 5.
WD 7.
Last annotation update !
                                                        Saccharomyces cerevisiae (Baker's yeast).
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72835 MW;
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EMBL; L26505; AAA96717.1; -.
PIR; S49932; S49932.
SGD; S0001308; MET30.
InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
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44408
44408
5338
6328
15-SEP-2003 (Rel. 42,
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
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607
61
640 AA;
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Churcher C.M., Bow
Chillingworth T.,
                  MET30 protein.
MET30 OR YIL046W.
                                                                                                                 NCBI TaxID=4932;
                                                                                                                                                                              STRAIN=X2180-1A;
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CONFLICT
SEQUENCE
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17.
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                                                                                                                                                                                                                                                                                                                                                                                152 GLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERR- 210
                                                                                                                                                                                                                                                                                                                                                                                                                                         --OELSLKÍLSYLDCOSLCNÁTRÝCRKWOKLADDBRVWYHMCEOHI------DRKC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 ---GWGQYLFKNK-----PPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQ 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 PNCGWGLPLLHMKRARIQQNSTGSSSNADIQTQTTRPWKVIYRERFKVESNWRKG---- 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIHCRSETSK----GVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQ 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 --HCKIQEFKGHMDGVLTLQFNYRLLFTGSYDSTIGIWDLFTGKLIRRLSGHSDGVKTLY 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDM 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 FÜDRKLITGSLDKTIRVWNYITGECISTYRGHSDSVLSVDSYQKVIVSGSADKTVKVWHV 409
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                                                                                                                                                                                                                                                        92 ASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPAR 151
                                                                                                                               34 IPEKNSLRQTYNSCARLCLN-QETVCLASTAMKTENCVAK-TKLANGTSSMIVPKQRKLS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            466 VOKITPLTIKDVENLATDNTSDGSSPQDDPTMTDGADESDTPSNEQETVLDENIPYPTHL
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STRAIN=14-07023-1A FGSC 987;
MEDLINE=95241499; PubMed=7724564;
Kumar A., Paietta J.V.;
The sulfur controller-2 negative regulatory gene of Neurospora crassa encodes a protein with beta-transducin repeats.";
Proc. Natl. Acad. Sci. U.S.A. 92:3343-3347(1995).
-!-FUNCTION: NEGATIVELY REGULATES SULFUR STRUCTIVALA GENE EXPRESSION.
-!- INDUCTION: EXPRESSED CNLY UNDER LOW-SULFUR CONDITIONS.
-!- SIMILARITY: Contains 1 F-box domain.
-!- SIMILARITY: BELONGS TO THE MET30/SCONB/SCON-2 FAMILY OF WD-REPEAT PROTEINS.
                                                                                                                                                                                        LPEYNFIKFCYRHNPDIQFSPTHTACYKQDLKRTQEINANIAKLPLQEQSDIHHIISKYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375 ASPIDITLRRVLVGHRAAVNVVDFDDKY1--VSASGDRTIKVWNTSTCEFVRTLNGH---
                                                                   Gaps
                                                                   124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
   Length 640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 504 RAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTI 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----KCMHTF---NGR--RLORETOHTOTOSLGDKV 609
                                                               85; Mismatches 202;
18.0%; Score 545; DB 1; 28.9%; Pred. No. 1.3e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FSB-2003 (Rel. 41, Last annotation update)
SCON-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                430 KRGIACLQYRD--RLVVSGSS
                                                               Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                 Similarity
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   Query Match
                                    Best Local
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510 LCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDF 546
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WD 3.
WD 4.
WD 5.
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InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
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Matches 150; Conservative
                                                                                                                                         STANDARD;
                                                                                                                                                                                                                           Sel-10 protein.
SEL-10 OR FSSB12.3.
Caenorhabditis elegans.
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493
579 AA;
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                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                         CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 VÝ----RDRWQVSYNWKNSRYKĽSVL---KGHENĠVTCĽQLDDNILATĠSYDTTÍKÍWNI 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    355 FINIGHMATCSKDRSIAVWDMASPIDITLRRVLVGHRAAVNV--VDFDDKYIVSASGDRTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413 KVWNTSTCEFVRTLNGHKRGI-------ACLQYRDRLVVS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               498 MSHAQIERAGSPGSHSSSHNLLPSSLPSGDEDVRHLYGSAFVADESRPLPPRYFMTGGLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177;
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DOMAIN 124 170 F-BOX.
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                                                                                                                                17.5%; Score 531.5;
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360
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881
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Matches 144;
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Rhabditidae, Peloderinae, Caenorhabditis.
NCBL TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones S.J.M.;
Submitted (JTL-1998) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: Contains 1 F-box domain.
-!- SIMILARITY: Contains 7 WD repeats.
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609 KCDATYTGHCGPVTCVGLSDSLMASGSEDGTIRLHSF 645
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15-DEC-1998 (Rel. 37, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
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Pfam; PP00400; WD40; 7.
Probom; PP000400; WD40; 7.
Probom; PP000018; WD40; 3.
SMART; SM00256; FBOX; 1.
PROSITE; PS50181; PBOX; 1.
PROSITE; PS50181; PBOX; 1.
PROSITE; PS500878; WD_REPEATS 1; 5.
PROSITE; PS50082; WD_REPEATS 1; 5.
PROSITE; PS50084; WD_REPEATS 1; 7.
PROSITE; PS50084; WD_REPEATS 1; 7.
PROSITE; PS50084; WD_REPEATS 1; 7.
PROSITE; PS50084; WD_REPEATS REGION; 1.
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us-09-601-168b-2.rsp

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PRINTS; PR00320;
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                                                                                                                                                                                                                                                                                                                     WDVNTGEMINTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPIDITLRRVLVGHRA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450 NTIRLWDI---ECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAP 506
  FVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELV 175
                                                                                                                                                                                                                                                                                                                                                                                                                        Shieh J.C., White A.M., Rosamond J.;
Submitted (Apr.196) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: THIS PROTEIN IS ESSENTIAL FOR INITIATION OF DNA
REPLICATION AND SEPARATION OF THE SPINDLE POLE BODIES TO FORM THE
POLES OF THE MITOTIC SPINDLE. IT ALSO PLAYS A ROLE IN BUD
DEVELOPMENT. FUSION OF ZYGOTIC NUCLEI AFTER CONJUGATION AND
VARIOUS ASPECTS OF SPORULATION. REQUIRED FOR HTAL-HTB1 LOCUS
TRANSCRIPTION ACTIVATION (BY SINILARITY).
-!- SIMILARITY: Contains 7 WD repeats.
                                 RIDSLWRGLAERRGWGQYLFKNKPPDGNAP
                                                                                                                                                                                           PN-SFYRALYPKIIQDI-------ETIBSNWRCGRHSLQRIHCRSETSKGVYCL
                                                                                                                                                                                                                                                                                        OYDDOKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLOYDE--RVIITGSSDSTVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      392 AVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDR--LVVSGSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 AVRCVQFDGTTVVSGGYDFTVKIMNAHTGRCIRTLTGHNNRVYSLLFESERSIVCSGSLD
                                                                                                                                            SKNWKLISEIDKIWKSLGVEBFKHHPDPTDRVTGAWQGTAIAAG-------VTIPDHIQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes, Saccharomycetales, mitosporic Saccharomycetales, Candida.
NCBI_TaxID=5476,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           484 EGT-CVHMLSGHRSAITSLOWFGRNWVATSSDDGTVKLWD 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTLCLRTLVEHSGRVFRLQ-FDEFQIVSSSHDDTILIWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CT-1996 (Rel. 34, Created)
CT-1996 (Rel. 34, Last sequence update)
EP-2003 (Rel. 42, Last annotation update)
division control protein 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   684 AA
                                                                                                  CKEWYRVTSDGMLWKKL - IERMV -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X96763; CAA65538.1; -. InterPro; IPR011810; F-box. InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001680; WD4
Pfam; PF004646; F-box; 1.
Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Candida albicans (Yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=SGY126
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15-SEP-2003
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CDC4 CANAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           339 HIFRGHISTIRCLDIIHPAVIGKNODGEDIVFPEYPLLITGSRDHNIHVWKLPVVDDSQD 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----AVLV 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 REWSTLPEINSAQVLYKK----RKIIVNRWMDPKFKPHRISVSGHGNKVVTCLQHDDEKV 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRA
                                                                                                                                                                                                                                                                                                                                                                                                                                   169 LCAAELVCKEWYRVTSDGMLWKKLIER--MVRTDSLWRGLAERRGWGQYLFKNKPPD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---GNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    459 YIETFEGEFDNPYLIAVLSGHTQSVRSISGYGNIIISGSYDSTVRVWDLLDDGHCTHVLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GH--RAAVNVVDFDDKYIVSASGDRIIKVNNTSTCEFVRTLNGHKRGIACLQYRDRLVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GHLDRVYSTAIDFHSKTCFSGSMDSNINVWNFETGELKKVLVGHASLVGLLDLVDDVLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKS
                                                                                                                                                                                                                                                                                                                                                                                            SEANONHLVFKLLQKTTRPTLSTFNNLINNSLKRDILSNVPF----EVTMKILSYLDYKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             506 PAGTLCLRTLVEHSGRVFRLQFD-----EFQIVSSSHDDTIL-IWDFLNDPAAQ 553
                                                                                                                                                                                                                                                                                                                        121; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Podospora anserina.
Bukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Lasiosphaeriaceae, Podospora.
                                                                                                                                                                                                                                                                                    DB 1; Length 684;
                                                                                                                                                                                                                                                                                                                        Indels
                                                                               Repeat; WD repeat
                                                                                                                                                                                                                                                3DD65DB31293B107 CRC64;
                                                                                                                                                                                                                                                                                  15.7%; Score 477.5; DB 1; 25.4%; Pred, No. 1.8e-28; ive 95; Mismatches 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Vegetatible incompatibility protein HET-E-1.
HET-E1.
                                                                                                                                                                         (POTENTIAL)
PROSITE; PSS0181, FEBX; 1.
PROSITE; PS00678; WD_REPEATS_1; 4.
PROSITE; PS50082; WD_REPEATS_2; 4.
PROSITE; PS50294; WD_REPEATS_2; 4.
Cell division; Mitosis; Sporulation; PS00AIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341 NTLIHH----CEAVLHL----RFNNG-
                                                                                                                                   WD 2.
WD 4.
WD 5.
WD 5.
                                                                                                                                                                                                                                                76090 MW;
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Matches 136; Conservative
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431
468
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549
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[1]
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us-09-601-168b-2.rsp

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MEDLINE=21948401; PubMed=11859360;

Med V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Squoros J., Peat N., Hayles J., Basham D., Bowman S.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gonlins M., Connor R., Cronin A., Davis P., Hidalgo J., Hodgson G.,

Holroyd S., Hornsby T., Hewarth S., Hutckle E.J., Hunt S., Jagels K.,

Monory P., Moules S., Mungall K., Mutphy L., Niblett D., Odell C.,

Monory P., Woule S., Mungall K., Mutphy L., Niblett D., Odell C.,

A nonory P., Noules S., Saunders D., Seeger K., Sharp S.,

Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitchead S.,

Rodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Nodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Nodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Religns I., Vanstreels E., Rieger M., Schaefer M., Mullbert H.,

Raper P., Zimmerrann W., Wedler H., Reinhardt R., Pohl T.M.,

Eggr P., Zimmerrann W., Wedler H., Mambutt R., Purnelle B.,

Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

Lucas M., Rochet M., Gaillardin C., Moore K., Hurst S.M.,

Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

A shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

Nature 415:871-880(2002).
"Fission yeast WD-repeat protein popl regulates genome ploidy through ubiguitin-proteasome-mediated degradation of the CDK inhibitor Rum1 and the S-phase initiator CG18,"; genes Dev. 11:1548-1560(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kominami K.-I., Ochotorena I., Toda T.,
"Two F-box/WD-repeat proteins Popl and Pop2 form hetero- and homo-
complexes together with cullin-1 in fission yeast SCP (Skip-
cullin-1-F-box) ubiquitin ligase.",
Genes Cells 3:721-735(1998).
                                                                                                                                                                                     P00660; Q9PPP3;
15-JUL-1998 (Rel. 36, Lested)
15-JUL-1998 (Rel. 36, Last sequence update)
26-FB2-2003 (Rel. 41) Last annotation update)
27-FB2-2003 (Rel. 41) Last annotation update)
38-FB2-2003 (Rel. 41) Last sequence (Pission yeast)
38-FB2-2003 (Pingi, Ascomycotates; Schizosaccharomycetes; Schizosaccharomycetes; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION MEDLINE=22325332; Pubmed=12167173;
                                                                                                                                                                            775 AA
                                                                                        1150 VASGSIDGTIKIWDAASGTCTO 1171
                                                      532 IVSSSHDDTILIWDFLNDPAAQ 553
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MEDLINE=97347242; PubMed=9203581;
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                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kominami K., Toda T.;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the RWBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 TGHTGSVLCLQY--DERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFN-NGMM 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   922 EGHGGRVQSVAFSPDGQRVASGSDDHTIKIWDAASGTCTQTLEGHGSSVLSVAFSPDGQR 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STCEFVRTLNGHKRGIACLQYR--DRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRC 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          476 IRF -- DNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLOF -- DEFQ 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        802 APIDSMIKKIFKKEEPGWISTISVVEAEWNACTQTLEGHGSSVLSVAFSADGQRVASGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ETSKG-------VYCLQY--DDQKIVSGLRDNTIKIWDKNTLECKRIL
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                                                                                                                                          GENE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 APPNSFYRALY----PKIIQDIETIESNWRCGRHSL---------ORIHCRS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66; Gaps
              MEDLINE=96009891; PubMed=7557402;
Saupe S., Turcq B., Begueret J.;
"A gene responsible for vegetative incompatibility in the fungus
Podospora anserina encodes a protein with a GTP-binding motif and
beta homologous domain.";
beta homologous (11954).
-!- PUNCTION: RESPONSIBLE FOR VEGETATIVE INCOMPATIBILITY THROUGH
SPECIFIC INTERACTIONS MITH DIFFERENT ALLELES OF THE UNLINKED G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.0%; Score 455.5; DB 1;
larity 31.7%; Pred. No. 2e-26;
Conservative 64; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTP (POTENTIAL).
WD 1.
WD 3.
WD 4.
WD 5.
WD 6.
WD 7.
WD 7.
                                                                                                                                                                            -!- SIMILARITY: Contains 10 WD repeats.
-!- SIMILARITY: Contains 1 NACHT domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0320; GPROTEINBRPT.
PRODON; PRO00320; MAD40; 10.
PROSITE; PS50837; NACHT; 1.
PROSITE; PS06087; NACHT; 1.
PROSITE; PS06087; NACHT; 1.
PROSITE; PS06082; WD REPEATS 1; 10.
PROSITE; PS50082; WD REPEATS 2; 10.
PROSITE; PS50294; WD_REPEATS 2; 10.
                                                                                                                                                                          SIMILARITY: Contains 10 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MD 2.
MD 3.
MD 5.
MD 5.
MD 7.
MD 8.
MD 9.
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InterPro; IPR001680; WD40.
Pfam; PP00400; WD40; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat; WD repeat.
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PIR; T18521; T18521.
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1205
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1175 120
1217 124
1356 AA;
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Local St
121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                    RHSLQRIHCRSETSKGVYC---LQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSV 310
                                                                                                                                                                                                       311 LCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIA 370
                                                                                                                                                                                                                                                                                                                                                                                                      ------TSTCEFVRTLNGHK---RGIACLQYRDRLVVSGSSDNTIRLWDIECGAC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRVLEGHEELVRCIRFDNKR--IVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSG 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PERSONAL STATE STA
                                                                                                                         390 LHAPEKIKRCSFPIHGVRLITKLOFDDDKIIVSTCSPRINIYDTKTGVLIRSLEEHEGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 553 NPDONNDFTSATTNPFYIRTLRGHTDSVRBVACL---GDLIVSASYDGTLRVWKASTGVC
                                                                                                                                                                                                                                                                    450 WTFEYVGDILVTGSIDRTVRVWDLRTGECKQVFYGHTSTIRCIKIVQGNQSTIDID----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRANIE-8288C, A BB972;
MUTAKAMI Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
Yamazaki M., Tashiro H., Eki T.;
Analysis of the nucleotide sequence of chromosome VI from
                                                                                                                                                                                                                                                                                                                                                     371 VWDMASPIDIILRRVLVGHRAAVNVVDFDDKYIVSASGDRIIKVWN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             661 LVSQVTFNQNILVSASAPPDTSLRVWD 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVFRLQFDEFQIVSSS--HDDTILIWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1988 (Rel. 04, Created)
01-NOV-1995 (Rel. 32, Last sequen
15-SEP-2003 (Rel. 42, Last annota
Cell division control protein 4.
CDC4 OR YFL009W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a related pseudogene.";
J. Mol. Biol. 195:233-245(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nat. Genet. 10:261-268(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 ITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYR-VTSDGMLWKKL-----I 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---CAIMKRVYFRHFNLRERW--- 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
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                                                                                                                                                                                               PUNCTION: Involved in maintenance of ploidy through proteasome dependent degradation of CDK inhibitor ruml and S-phase initiator cdc18. Functions as a recognition factor for ruml and cdc18, which are subsequently ubiquitinated and targeted to the 26S proteasome for degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 REKCLKRRNSSLSSNLHANKRFLFNSQSDGNKKNETFPSTNYSNVFYPNNCDSKEVASET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 TFSLDAPMNSVNYSYPSPNLLGNDSKTRQSFPPHSSSSSHNSLHEPVIYDFSSENPSIHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 ERMVRIDSLWRGLAERRGWGOYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 QEKALKFMNSSEREDC------NNGEPPRKIIPEKNSLRQTY-NSCARLCLNQST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 VC-----LASTAMKTENCVAKTKLANGTSSMIVPKORKLSA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----SYEKEKEL----CVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Homodimer and heterodimer with pop2. Binds to pcul, pip1
Seibert V., Prohl C., Schoultz I., Rhee E., Lopez R., Abderazzaq K.,
Zhou C., Wolf D.A.;
                                            Zhou C., Wolf D.A.;
"Combinatorial diversity of fission yeast SCF ubiquitin ligases by
homo-and heterooligomeric assemblies of the F-box proteins Poplp ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86; Mismatches 229; Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B06EDBA46553EEC1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 F-box domain.
-!- SIMILARITY: Contains 5 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50181; FBCX; 1.
PROSITE; PS0678; ND REPBAIS 1; 3.
PROSITE; PS50082; ND REPBAIS 2; 4.
PROSITE; PS50294; WD_REPBAIS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat.
F-BOX.
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MD 3.
MD 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               and cdc18.
SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y08391; CAA69671.1; -.
EMBL; AL022103; CAA17898.1; -.
EMBL; AL157874; CAB75991.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; T45136; T45136.
GeneDB SPombe, SPR-118.01; --
InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00320; GPROTEINBRPT.
SMART; SM00256; FBOX; 1.
SWART; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87816 MW;
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DSKIRTMCLEQSLSA----
                                                                                                                                                              Pop2p.";
BMC Biochem. 3:22-22(2002).
-!- FUNCTION: Involved in mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 162; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF00646; F-box, 1.
Pfam, PF00400; WD40; 6.
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MEDLINE=21848401; PubMed=11859360;
WEDLINE=21848401; PubMed=11859360;
Wed V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., As Squaros J., Peat N., Hayles J., Basham D., Bowans S., Brown D., Brown S., Chillingworth T., Churcher C.M., Brown D., Brown D., Harris D., Hiddenl T., Fraser A., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Androws S., Goble A., Hamin N., Harris D., Hiddenl T., Fraser A., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Androwy S., Money P. Money P. Money P. Money P. Money P. Money P. Money R., Parison D., Quail M.A., Rabbinowisch E., Antherford K., Rutter S., Saunders D., Seeger K., Sharp S., Stevens K., Stevens K., Antherford K., Rutter S., Saunders D., Stevens K., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Achter S., Stevens R., Schaefer M., Mueller Aner S., Gabel C., Fuchs M., Fritzc C., Holzer E., Mooset ID., Hilbert H., Achter S., Gloux S., Lelaure V., Mortier S., Goffeau A., Cadieu B., Dreano S., Gloux S., Lelaure V., Mortier S., Animatron J., Noren E., Moren S., Lunca M., Rollardin C., Moren S., Armstrong J., Forsburg S.L., Applakovski G.V., Ussery D., Barrell B.G., Nurse P.; The Sequence Square R., Revuelte J., Moren S., Armstrong S., The Schole M., Schaefer M., Schaefer M., Schaefer M., Schaefer M., Schaefer M., Gallardin C., Taylor Barrell B.G., Nurse P.; Thode G., Shakovski G.V., Ussery D., Barrell B.G., Nurse P.; The Schaefer M., 
                                       SMDTTIRIWDLENIWANGECSYATNSASPCAKILGAMYTLOGHTALVGLIRLSDKFLVSA 648
    487 AYDGKIKVWDL------VAALDPRAPAGTL--CLRTLVEHSGRVFRLQFDEFQIVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins for degradation and stops unwanted diploidization in fission
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BEDILME-SAB1862B, PubMed=9653157;

Jallepalli P.V. Tien D., Kelly T.J.;

"sudl+ targets cyclin-dependent kinase-phosphorylated Cdc18 and Ruml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99227353; PubMed=10209119;
Wolf D.A., McKeon F., Jackson P.K.;
F-Dox/Morrepeat proteins popp and Sudip/Pop2p form complexes that
bind and direct the proteolysis of cdc18p.";
Curr. Biol. 9:373-376 (1999).
                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
POP2 OR SUDI OR SPAC4D7.03.
POP2 OR SUDI OR SPAC4D7.03.
Subsarcharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetales;
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                                                                                                                          668
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                                                                                     SHDDTILIWDFLNDPAAQAEPPRSPSRTYTY
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MEDLINE≈99144318; PubMed=9990507;
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NCBL_TaxID=4896;
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                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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      in no
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Repeat; WD repeat; 3D-structure.
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      as its content
                                                                                                EMBL, X05625; CAA29113.1; -.
EMBL, D50617; BAA09229.1; -.
EMBL, Z46555; CAA66341.1; -.
PTR, S56245; S36245.
PDB, 110EX, 18-PEB-03.
SGD, S0001885; CDC4.
GO, GO:0000082; P:G1/S transition of mitotic cell cycle; GO; GO:000086; P:G2/M transition of mitotic cell cycle; InterPro; IPR001810; F-box.
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0348F2F8FA78F3BC CRC64;
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WD 2.
WD 3.
WD 4.
WD 5.
WD 6.
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les 139; Conservative
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79 AA;
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                                                                                                                                                                                                                   FUNCTION: Involved in maintenance of ploidy through proteasome dependent degradation of CDK inhibitor ruml and S-phase initiator cdc18. Functions as a recognition factor for ruml and cdc18, which are subsequently ubiquitinated and targeted to the 265 proteasome for degradation.
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                                                                                          FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
MEDLINE=22325332; PubMed=12167173;
Seibert V, Prohl C., Schoultz I., Rhee E., Lopez R., Abderazzag K.,
Zhou C., Wolf D.A., "Combinatorial diversity of fission yeast SCF ubiquitin ligases by
homo-and heterooligomeric assemblies of the F-box proteins Poptp and
                                                                                                                                                                                                                                                                                                  SUBUNIT: Homodimer and heterodimer with popl. Binds to pcul, pipl
Kominami K.-I., Ochotorena I., Toda T.,
"Two F-box/WD-repeat proteins Popl and Pop2 form hetero- and homo-
complexes together with cullin-1 in fission yeast SCF (Skip-
cullin-1-F-box) ubiquitin ligase.";
Genes Cells 3:721-735(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 703;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.1%; Score 396.5; DB 1; Length '23.3%; Pred. No. 2.46-22; ive 92; Mismatches 226; Indels
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                                                                                                                                                                                                                                                                                                                                  cytoplasmic.
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PRODOM; PD000018; WD40; 1.
SMART; SM00256; FEDX; 1.
SMART; SM00320; W040; 7.
PROSITE; PS50181; PBOX; 1.
PROSITE; PS500878; WD_REPEATS 1; 3.
PROSITE; PS500879; WD_REPEATS 2; 6.
PROSITE; PS500879; WD_REPEATS 2; 6.
Nuclear protein; Repeat; WD_Tepeat.
                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Nuclear, and cy
-!- SIMILARITY: Contains 1 F-box domain.
-!- SIMILARITY: Contains 6 WD repeats.
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F-BOX.
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79605 MW;
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InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
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Pfam; PF00400; WD40; 6.
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703 AA;
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268 TWNRILDVHTS---YWKHMF-----SLFGFQINENDW----KYANPNLNRPPFLHND 312
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October 22, 2003, 10:06:36; Search time 84 Seconds (without alignments) 1075.184 Million cell updates/sec A Geneseq 197un03:\*

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| SIDSI/gcgdata/geneseq\_genesegp 3034 1 MDPAEAVLQEKALKFMNSSE......PAAQAEPPRSPSRTYTYISR 569 1107863 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. Total number of hits satisfying chosen parameters: 1107863 segs, 158726573 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM protein - protein search, using sw model Gapop 10.0 , Gapext 0.5 Ainimum DB seq length: 0 Aaximum DB seq length: 20000000000 US-09-601-168B-2 **BLOSUM62** Perfect score: scoring table: Jatabase : sequence: searched: Run on:

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SUMMARIES		Ę		AAY24054	AAB12813	AAY96697	AAY83041	AAY83250	AAY44249	AA022446	ABG69473	AAB48298
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## ALIGNMENTS

RESULT 1

Beta-transducin repeat containing protein; beta-TrcP; Skplp; processome degradation pathway; Vpu protein; beta-catenin; human immune defliciency virus-1; HIV-1; cellular protein; IKappaB; ubiquitinylation; phosphorylated protein; tumour; apoptosis; Alzheimer's; antiviral; antitumour; cell cycle regulation; protein degradation; and anti-inflammatory; osteo-articular inflammation; acute inflammation; tumour necrosis factor. A human beta-transducin repeat containing protein. "F box sequence" Location/Qualifiers AAY24054 standard; Protein; 569 AA. /note= "WD motif" 343..372 'note= "WD motif"
187..415
'note= "WD motif" "WD motif" (updated)
(first entry) /note= "F 259..292 104..332 147..191 'note= Homo sapiens 20-MAR-2003 30-SEP-1999 AAY24054; Key Region Region Region Region Region  ~

420

Region Region

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The present invention describes an F-box motif protein of ubiquitin ligase SCF complex which promotes the ubiquitination of IkappaB or beta-catenia and is constituted by Skpl protein, cull protein and a complex (SCF complex) of Fox protein containing F-box motif and WD40 repeat motif and has the amino acid sequence of 45 residues (AAB12811) or one of two 569 residue sequences (AAB12812, which is mouse ubiquitin ligase FWD1 protein) and (AAB12813, which is man beta-transducin repeat containing protein (Deta-TroE). The F-box protein can be used for the gene therapy of colon cancer by being recombined to a virus vector.
RILICHIGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMM 360
                                                                                                                       RILIGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGBMLNTLIHHCEAVLHLRFNNGMM 360
                                                                                                                                                                                                                      VICSKDRSIAVWDMASPIDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC 420
                                                                                                                                                                                                                                                                                                         EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN 480
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                                                                                                                                                                               VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC
                                                                                                                                                                                                                                                                       421 EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN
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N-PSDB; AAA73132.
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516..544
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Local Similarity 100.
es 569; Conservative
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Human beta-TrCP, an F-box/WD protein family member, has been shown to have homology to human E3 ubiquitin ligase (E3). E3 enhances ubiquitination of phosphorylated I-kappa-B, an inhibitor protein of nuclear factor kappa-B (NF kappa-B). Understanding I-kappa-B degradation via the ubiquitin pathway is useful for identifying modulators of this process for use in treating diseases associated with activation of NF kappa-B. In vitro analysis suggests that deletion of the F-box results in a protein that functions as a dominant negative molecule in vivo. Translent over-expression of edica-beta-TrCP (a deletion mutant) inhibited the degradation of endogenous I-kappa-B-alpha in stimulated Jurkat cells, resulting in accumulation of phosphorylated I-kappa-B-alpha -B can be used to screen for modulate NF-kappa-B to treat inflammatory diseases, autoimmune diseases, cancer and viral infections.
                                                                                       Polypeptide enhancing phosphorylated lkappaB ubiquitination useful for treating disorder associated with NF-kappaB activation e.g. cancer, comprising amino acid sequence of human E3 ubiquitin ligase or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGWM
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Matches 569; Conservative
                           WPI; 2000-431294/37
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                                                                                                 MPPABAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA
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                           Indels
  Pred, No. 2.5e-286;
Mismatches 0;
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SS ) YISSUM RES & DEV CO.
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                         nes 569, Conservative
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Local Similarity
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RVTSDGMLWKKLIERMVRIDSLWRGLAERRGWGQYLFKWKPPDGNAPPNSFYRALYPKII
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                                                                  QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Targeting degradation of polypeptide useful for treating cancer and other proliferative disorders, involves conjugating polypeptide with ubiquitin protein ligase or inhibiting ubiquitination using organic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ubiquitin ligase; SCF; F-box protein; targeted degradation; destabilisation; proteolysis; drug discovery; gene therapy; cancer; oncoprotein; Huntington's disease; gene knockout; delivery systems;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vel nucleic acid for screening compounds useful for treating oliferative and differentiative disorders such as cancer and immune sorders comprises sequences encoding ubiquitin ligases
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                                                                                                                                                                                                                     box protein; FBP; diagnosis; treatment; screening; agonist; itagonist; proliferative disorder; differentiative disorder; cast cancer; cancer; cancer; cancer; all cell lung carcitnoms; immune disorder; cardiovascular disorder; flammatory disorder; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cleic acids encoding substrate-targeting subunits of ubiquitin gases with F-box motifs (F-box proteins) are useful for diagnosis proliferative and differentiated related disorders by measuring sense expression. Calls expressing such proteins or air fragments are useful for screening compounds. The compounds agonists or antagonists, which are useful for treating a biferative or differentiative disorder in a mammal such as ast, ovarian and prostate cancer and small cell lung carcinoma lalso major opportunistic infections, immune disorders, diovascular diseases and inflammatory disorders. FBP protein, logs, derivatives and their subsequences, anti-FBP antibodies also useful in diagnosis of the disorders.
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-MAR-1999;
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Homo sapiens

0 120 180 180 240 300 300 360 360 420 420 480 480 09 09 preasing the level of a target polypeptide and for creating and expressing a destabilized polypeptide which is subjected to SCF sediated proteolysis. Degrading any desired protein in a cell is set of preventing or treating diseases caused by the presence of mormal amount of the specific polypeptides, for drug diseovery and its gene therapy. Diseases treated include cancer, by degradation of icoproteins, Huntington's disease, other proliferative disorders and croproteins. The method provides a quick and easy its changes in the method provides a quick and easy leterative to gene knockout technology. The traget polypeptide can degraded at all stages, or a specific stage, of development in the 1 MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNOETVCLA STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKYFEOWSESDOVEFVEHL STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKYFEOWSESDOVEFVEHL ISOMCHYOHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII QDIETIESNWRCGRASLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK QDIBTIBSNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK RILIGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMM RILIGHIGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMINTLIHHCEAVLHLRFNNGMM VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC VICSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC **EPVRTLNGHKRGIACLOYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN** EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN KRIVSGAYDGKIKWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT ISOMCHYOHGHINSYLKPMLORDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY Gaps . 0 100.0%; Score 3034; DB 21; Length 569; 100.0%; Pred. No. 2.5e-286; tive 0; Mismatches 0; Indels 0; 569 ILIWDFLNDPAAQAEPPRSPSRTYTYISR ILIMDFLNDPAQAEPPRSPSRTYTYISR Local Similarity 100. es 569; Conservative 569 AA sture animal. adnence 19 61 121 181 241 241 301 421 481 481 541 181 301 361 361 421 / Match

744249 standard; Protein; 569

FEB-2000 (first entry

nan cell signalling protein-12.

l signalling protein-12; CSIGP-12; cell proliferation; lammatory disorder; cirrhosis; cancer; hepatitis; AIDS; eriosclerosis; Addison's disease; multiple sclerosis.

Patterson C; "Potential phosphorylation site" site" "Potential phosphorylation site" site" site" site note= "Potential glycosylation site" "Potential glycosylation site" "Potential phosphorylation "Potential phosphorylation ΥT, "Potential phosphorylation phosphorylation "Potential phosphorylation note= "Potential glycosylation Tang 360..374 /label= Signature\_sequence 403..417 /label= Signature\_sequence 483.497 /label= Signature\_sequence 532..546 /label= Signature\_sequence 320..334 /label= Signature\_sequence /label≈ Signature sequence Yue H, Location/Qualifiers "Potential ď Lal 98US-0085343 99WO-US10567 .457 INCY-) INCYTE PHARM INC Hillman JL, note= /note= 451 'note= note= 'note= WPI; 2000-086432/07. N-PSDB; AAZ29233. Yang J; Key Modified-site 13-MAY-1999; 409958558-A2 13-MAY-1998; 26-AUG-1998; 18-NOV-1999 Bandman O, Baughn MR, Region Region Region Region Region Region  Cytostatic; immunomodulator; cardiant; antiinflammatory; antimicrobial;

SEQ ID

Human F-box protein FBP1

proliferative, differentiative disorder; Skp2; F-box protein; cancer; ubiquitin ligase; breast cancer; prostate cancer; ovarian cancer; small cell lung carcinoma; immune disorder; parathyroid adenoma; FBP; infiammatory disorder; lymphoma; major opportunistic infection; certain cardiovascular disease; human.

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he present sequence is cell signalling protein-12 (CSIGP-12) encoded y cDNA obtained from Incyte clone 323949 of COLANCTO1 library. It is xpressed in musculoskeletal, gastrointestinal and nervous tissues and is cond to be homologous to beta-transducin repeats containing rotein. Fragments of CSIGP encoding nucleic acid can be used as ariants. Recombinant CSIGP can be produced in host cells by transforming hem with generically appliered vectors. Agonists or allelic sed in the treatment of cell proliferative and inflammatory disorders secint with decreased or increased CSIGP expression. CSIGP is used in the dispension and treatment of cell proliferative and inflammatory disorders secint edangosis, prevention and treatment of cell proliferative disorders its days between the dispension of cell proliferative disorders is exercisely expression. CSIGP is used in the days of the dispension of cell proliferative disorders is carried arteriosis, carrier, hepatitics and inflammatory is corders like AIDS, Addison's disease, multiple sclerosis, etc.
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e.g. diagnosing cell
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                uman cell signaling proteins useful for, roliferative and inflammatory disorders
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07-JAN-2002; 2002WO-US00311 05-JAN-2001; 2001US-260179P. (UYNY ) UNIV NEW YORK STATE.

Homo sapiens. WO200255665-A2

> 240 360 540 240 420 480 EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN 480 540 180 180 QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK 300 QDIBTIESNWRCGRHSLQRIHCRSBTSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK 300 VICSKDRSIAVWDMASPIDITLRRVLVGHRAAVMVVDFDDKYIVSASGDRTIKVWNTSTC 420 121 ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII RILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMM KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLOFDEFOIVSSSHDDT 121 ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569 ILIWDFLNDPAAQAEPPRSPSRTYTYISR 181 181 241 301 361 361 421 481 541 241 301 421

The invention relates to screening compounds useful for the treatment of proliferative or differentiative disorders comprising detecting a change in the activity of Skp2 (F-box protein). The method is useful for screening compounds for the treatment of proliferative or differentiative disorders, particularly cancer. These compounds include small molecules, or compounds or derivatives or analogues of the new ubiquitin ligases. The compounds are useful for treating diseases such as cancer (e.g. breast cancer, prostate cancer or ovarian cancer, lymphoma, small cell lung cardinoma or parathyroid adenomas), major opportunistic infections, immune disorders, certain cardiovascular diseases or inflammatory disorders. This sequence represents an F-box protein (FBP) relating to

569 AA;

Sequence

Screening compounds for treating proliferative disorders, e.g. breast cancer or prostrate cancer, infections or immune disorders, comprises detecting a change in the activity of Skp2 with either p27 or Cks1

WPI; 2002-599665/64.

Pagano M;

N-PSDB; AAL41041

Disclosure; Fig 3; 246pp; English

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  DB 23;
; Score 3034; DB 23;
; Pred. No. 2.5e-286;
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Query Match
Best Local Similarity 100.
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(first entry)

OCT-2002

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Gaps

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Length 569; Indels 120

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361 421 121 481 481

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the protein-protein interactions and useful for treating obsetty and metabolic disorders e.g. non-insulin dependent diabetes mellitus, by DDM. The compound isolated by the method is useful for treating and preventing obsetty or metabolic diseases. The interactions between the proteins of the complex further define a set of selected interacting domains, SID. The present sequence represents a member of the protein hybrid assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVTSDGMLWKKLIBRMVRIDSLWRGLABRRGWGQYLFRNKPPDGNAPPNSFYRALYPKII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RILIGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISOMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA
                                                                                                                                                                                                                        in the specification but
                                                                                                                                                                                                                     Note: The present sequence was not displayed in the was obtained from its Genbank entry by the indexer
  The complexes are useful for identifying
                                                                                                                                                                                                                                                                                                                                              ; Score 3034; DB 23;
; Pred. No. 2.5e-286;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 569; Conservative
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                                                                                                                                                                                                                                                                                                 569 AA;
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                                                                                                                          420
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                                                                                                                                                                                                                                                                                                         KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDBFQIVSSHDDT
                            RILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMM
                                                                                                                          VICSKDRSIAVWDMASPIDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRIIKVWNTSIC
                                                                                                                                                                              EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN
                                                                                                                                                                                                           KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
                                                                                VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC
vel complex of protein-protein interactions in adipocyte cells for entifying compounds that modulate the protein-protein interactions i useful for treating obesity and metabolic disorders -
                                                                                                                                                                                                                                                                                                                                                                          ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                                                                                                                                                                                                                                                                                                                                                       ILIWDFINDPAAQAEDPRSPSRTYTYISR 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G69473 standard; Protein; 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              man bait protein beta-TrCP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DEC-2001; 2001WO-EP15423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -JAN-2001; 2001US-259377P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aim 1; Page -; 125pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YBR-) HYBRIGENICS.
ARS ) CENT NAT RECH
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>SDB; ABS51009.
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mo sapiens

-JUL-2002

grain P,

-OCT-2002

G69473;

541

480

; Ic

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Score 3027;
Pred. No. 1.
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                                                                                                                          AAM00960 standard; Protein; 608
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2000US-0552317.
2000US-0598042.
2000US-0620312.
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2000US-0693036.
2000US-0250583.
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                                                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-2000; 2000WO-US34960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0653450
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Werhman T
                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488707/53.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-APR-2000; 2
09-JUL-2000; 2
19-JUL-2000; 2
03-AUG-2000; 2
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                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-2000;
                                                                                                                                                                                   01-OCT-2001
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                           541
                                                                                                                                                       AAM00960;
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                                                                                                                                                                                                                                                                                                                       le invention relates to methods of altering the polypeptide levels in a all, using proteins selected from S-phase kinase associated proteins 1 d 2 (SRP1, SRP2), SRP2-like proteins (STB) and CUL-1 (a member of the illin/ CDC53 family of proteins). The method is useful for altering the vel of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or BG1-2 ) Mypeptide in a cell. SRP2 and SKP2-like protein levels are useful for tecting tumours, and in monitoring tumor treatment in a mammal. Agents eating tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VICSKDRSIAVWDMASPIDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRIIKVWNTSIC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STAMKTENCVAKTKLANGTSSMIVPKORKLSASYBKEKELCVKYFEOWSESDQVEFVEHL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDIETIESNWRCGRHSLORIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MDPAEAVLQEKALKFWNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60
                                                                                                                                                                                                                                       odulating polypeptide levels in a cell, diagnosing and treating tumor, wolves altering levels of proteins such as S-phase kinase associated coteins 1, 2 and cullin/CDC53 proteins -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLOFDEFQIVSSSHDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGOYLFKNKPPDGNAPPNSFYRALYPKII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYBKEKELCVKYFEQWSESDQVEFVEHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 3027; DB 22; Length 569;
Pred. No. 1.2e-285;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                               laim 3; Page 130-132; 162pp; English.
                                                                                                                                                                    Kondo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.8%;
                                                                                5-JUN-2000; 2000WO-US15449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 99.8 es 568; Conservative
                                                                                                                                                                   lang H, Tsvetkov LM,
                                                                                                                                                                                              2001-061703/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      569 AA;
                                                                                                                                        JYYA ) UNIV YALE
                                                                                                                                                                                                            -PSDB; AAC84610
                           J200075184-A1
omo sapiens.
                                                                                                           1-JUN-1999;
                                                    4-DEC-2000
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481 KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, bone marrow, antiinflammatory, cytostatic, neuroprotective, antiviral, antibacterial, antifungal, anti-HIV, haemostatic, immunosuppressive, gene therapy, cytokine cell proliferation, cell differentiation modulator, immune disorder; infection, cancer; human immunodeficiency virus, HIV, autoimmune disorder; haemophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polynucleotide and polypeptide can used as nutritional sources or supplements and in the screening chemical compounds as potential drugs.
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Y, Zhang
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e AJ, Yang
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1.4e-285;
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ang J, Werhman T, Xu C, Xue AJ,
Zhou P, Drmanac RT;
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                                                                                                                                               Claim 10; Page 523-524; 648pp; English
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Length 608;

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SGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPR
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94.0%;
30-NOV-2000; 2000US-0728422
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Best Local Similarity 94.0
Matches 569; Conservative
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                                                                                                              WPI; 2001-476283/51.
N-PSDB; AAK51715.
                                                      Liu C, I
Wang D,
Yang Y, V
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                            (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                          inflammation.
                                                        Tang YT,
Zhao QA,
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                            9
                                                40 MDPVEAVLQEKALKFWNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA
                                                                                                  STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL
                                                                                                                                          121 ISOMCHYQHGHINSYLKPMLQRDFITALPARGLDHIABNILSYLDAKSLCAABLVCKEWY
                                                                                                                                                             ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIABNILSYLDAKSLCAAELVCKEWY
                                                                                                                                                                                                                                                                                                                  RILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMM
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                           MDPAEAVLQBKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA
                                                                                   STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL
                                                                                                                                                                                                  RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII
                                                                                                                                                                                                                             RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII
                                                                                                                                                                                                                                                                                                                                                                                                 VICSKORSIAVWDMASPIDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRIIKVWNISIC
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Gaps
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Indels
Mismatches
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-JUN-2000; 2000US-0598075.
-JUL-2000; 2000US-0654035.
-SEP-2000; 2000US-0654936.
-SEP-2000; 2000US-0654561.
-OCT-2000; 2000US-0693325.
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Conservative
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VLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVV 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78313-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other oytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoissis regulating activity, insue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
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        Мa
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                                                                                                                                                                                                                                                                                             Nucleic acids encoding polypeptides with cytokine-like activities,
        Cao Y,
ng ZW;
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                                       Wang
        Xu C,
R, Wa
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Drmanac RT, Asundi V, Zhou P,
Wang J, Zhang J, Ren F, Chen
Wejhrman T, Goodrich R;
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Pred. No. 1.5e-283;
0; Mismatches 0;
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120 144 180 204

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9 24

264 300 324 360 384 420

AB12812 standard; protein; 569

569 TYISR 605

TYISE

565 601

505

7-NOV-2000 (first entry)

AB12812;

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QD1ET1ESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNT1K1WDKNTLECK
                                                                                                 QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKSTLECK
                                                                                                                                                          RILIGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMM
                                                                                                                                                                                                301 RILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNAGEMLNTLIHHCEAVLHLRFNNGMM
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                                                                                                                                                                                                                                                                                                                                     EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRIVSGAYDGKIKVWDIMAALDPRAPAGTLCIRTLVEHSGRVFRLQFDEFQIVSSSHDDT
                                                                                                                                                                                                                                               VICSKDRSIAVWDMASPIDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRIIKVWNISIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Targeting degradation of polypeptide useful for treating cancer and other proliferative disorders, involves conjugating polypeptide with ubiquitin protein ligase or inhibiting ubiquitination using organic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin ligases) which can be used for the targetted degradation of a target polypeptide in vivo. Targetted degradation is achieved by expressing the ubiquitin ligase in a cell linked to the interaction domain of the target polypeptide and thereby recruiting the target polypeptide to the ubiquitin ligase. Such methods are useful for decreasing or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ubiquitin ligase; SCF; F-box protein; targeted degradation; destabilisation; proteolysis; drug discovery; gene therapy; cancer; oncoprotein; Huntington's disease; gene knockout; delivery systems;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILIWDFLNDPAAHAEPPRSPSRTYTYISR 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; Page 184-185; 185pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e present invention describes an F-box motif protein of ubiquitin gase SCF complex which promotes the ubiquitination of IkappaB or ta-carenin and a constituted by Skpl protein, cull protein and a mplex (SCF complex) of F-box protein containing F-box motif and WB40 peat motif and has the amino acid sequence of 45 residues (AAB12811) one of two 569 residue sequences (AAB12812, which is mouse ubiquitin gase FWDI protein) and (AAB12813, which is human beta-transducin egene therapy of colon cancer by being recombined to a virus vector.
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                              541 APAGTLCIRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDPAAQAEPPRSPSRTY 600
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  564
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                                                                                                                                                                                                                                                                                                                                                                                                                          oiguitin ligase SCF complex; F-box protein; ubiquitination; IkappaB; sta-catenin; Skp1; Cull; F-box motif; WD40 repeat motif; FWD1; and therapy; colon cancer; beta-transducin repeat containing protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA
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APAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT1L1WDFLNDPAAQAEPPRSPSRTY
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Pred. No. 1e-282;
                                                                                                                                                                                                                                                                                                                                                                               ouse ubiquitin ligase FWD1 protein SEQ ID NO:2.
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GAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN

2000-485550/43

PSDB; AAA73131

98JP-0343437.

-DEC-1998; )-JUN-2000.

22000166542-A.

sulusculus

aim 2; Page 9-10; 19pp; Japanese

3,

Conservative

Similarity

569 AA;

dnence

98.8%;

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noreasing the level of a target polypeptide and for creating and xpressing a destabilized polypeptide which is subjected to SCF seliated proteolysis. Degrading any desired protein in a cell is setul for preventing or treating diseases caused by the presence of bnormal amount of the specific polypeptides, for drug discovery and or gene therapy. Diseases treated include cancer, by degradation of ncoproteins, Huntington's disease, other proliferative disorders and croproteins. The method provides a quick and easy literative to gene knockout technology. The target polypeptide can edgraded at all stages, or a specific stage, of development in the
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569 AA; ednence

Gaps 0; 98.8%; Score 2997; DB 21; Length 569; 99.6%; Pred. No. le-282; ive 3; Mismatches 5; Indels 0 hes 561; Conservative Similarity y Match Local

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9 1 MDPABAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCINQETVCLT

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180 ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 180 ISOMCHYOHGHINSYLKPMLORDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWY 121

240 RVISDGMLWKKLIBRMVRIDSLWRGLABRRGWGQYLFKWKPPDGNAPPNSFYRALYPKII 181

240 RVTSDGMLWKKLIERWVRTDSLWRGLAERRGWGOYLFKNKPPDENAPPNSFYRALYPKII 181

420 VTCSKDRSIAVWDMASPIDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNISTC 361

481

540

ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569 541

iliwbelnbpaahaeppkspskryrysk

M78584 standard; Protein; 632

117 120

60 57

(first entry) -NOV-2001

nan protein SEQ ID NO 1246.

nan; cytokine; cell proliferation; cell differentiation; gene therapy; solare; peptide therapy; stem cell growth factor; haematopoiesis; subset growth factor; immunomodulatory; cancer; leukaemia; rvous system disorder; arthritis; inflammation.

EHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCK 240 CLASTAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKYFEOWSESDOVEFV 180 EWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYP 300 The invention relates to polynucleotides (AAKS1456-AAKS3435) and the encoded polypeptides (AAMY8323-AAM80320). That exhibit a cativity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodiatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and 2111 (AAK52582) and 3666 from the sequence listing 61 MPSLRCLYNPGTGALTAFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETV CLASTAMKTENCVAKTKLANGTSSMIVPKORKLISASYEKEKELCVKYFEQWSESDQVEFV BHLISOMCHYOHGHINSYLKPMLORDFITALPARGLDHIAENILSYLDAKSLCAAELVCK EWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYP 1 MDPABAVLQBKALKFMMEFRSWCPGWNTMARSRLTATSTSRVQCSMPRSLWLGCSSLADS --- FMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETV Gaps polypeptides with cytokine-like activities C, Cao Y, Wang ZW; 63; DB 22; Length 632; Indels Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu ( Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Xue AJ, Yang Y, Wejhrman T, Goodrich R; Score 2992.5; DB 22; Pred. No. 3.3e-282; 0; Mismatches 0; Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication. Claim 20; Page 3505-3507; 6221pp; English. Nucleic acids encoding polypeptides wuseful in diagnosis and gene therapy 98.6%; 2000US-0560875. 2000US-0598075. 19-JUL-2000, 2000US-0620325. 01-SEP-2000, 2000US-0654936. 15-SEP-2000, 2000US-0653561. 20-0CT-2000, 2000US-063335. 30-NOV-2000, 2000US-0728422. 2000US-0496914 05-FEB-2001; 2001WO-US04098 Conservative 1 MDPABAVLOEKALK-WPI; 2001-476283/51. 15 -----Similarity 632 AA; (HYSE-) HYSEQ INC. N-PSDB; AAK51717 WO200157190-A2 27-APR-2000; 20-JUN-2000; 19-JUL-2000; inflammation. Homo sapiens 03-FEB-2000: Best Local Sim Matches 569; Tang YT, Zhao QA, Sequence 181 58 121 118 178 Query Match g à g 셤 g ò ð à  $\delta$ 셤

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                      KIIQDISTIBSNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTL 360
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                                                                              ECKRILIGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNN
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AM79566 standard; Protein; 654

AM79566

uman protein SEQ ID NO 3212 (first entry) 5-NOV-2001

uman; cytokine; cell proliferation; cell differentiation; gene therapy; accine; peptide therapy; scem cell growth factor; haematopoiesis; issue growth factor; immunomodulatory; cancer; leukaemia; irvous system disorder; arthritis; inflammation.

smo sapiens

3200157190-A2

-FEB-2001; 2001WO-US04098

-FEB-2000; 2000US-0496914.
-APR-2000; 2000US-0560875.
-UUN-2000; 2000US-0590075.
-UUL-2000; 2000US-0630325.
-SEP-2000; 2000US-063561.
-SEP-2000; 2000US-063561.
-OCT-2000; 2000US-063325.

YSE-) HYSEQ INC.

Cao Y, C, Car Wang χ, κ chen Drmanac RT, Asundi V, Zhou Wang J, Zhang J, Ren F, C Wejhrman T, Goodrich R; Liu C, Wang D, Yang Y, ng YT, ao QA, e AJ,

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2001-476283/51 I; 2001-476283/ PSDB; AAK52699 cleic acids encoding polypeptides with cytokine-like activities, eful in diagnosis and gene therapy -

aim 20; Page 285-286; 6221pp; English

e invention relates to polynucleotides (AAK51456-AAK53435) and the coded polypeptides (AAM78323-AAM80302) that exhibit activity elating to

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cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissus growth factor activity, immunomodiatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.

Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 MPSLRCLYNPGTGALTAFQNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETV
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                                                                                                                                                                                                                                                                                                                                                                                             23 MDPABAVLOBKALKFMMEPRSWCPGWNTMARSRLTATSTSRVQCSMPRSLWLGCSSLADS
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US-09-213-688-6 US-09-328-877A-6 US-09-328-877A-5 US-09-328-877A-9 US-09-218-887-9 US-09-218-887-8 US-09-218-877A-9 US-09-218-877A-4 US-09-213-888-4 US-09-328-877A-4 US-09-318-877A-3 US-09-313-888-4 US-09-313-888-4 US-09-313-888-7 US-09-313-888-7 US-09-313-888-25 US-09-314-8506 US-10-128-714-3506 US-10-128-714-3506

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US-09-812-18

US 61 STAMKTENCVAKTKLANGTSSMIVPKORKLSASYEKEKELCVKYFEQWSESDOVEPVEHL 120 09 1 MDPAEAVLQEKALKFWNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 1 MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA Query Match 100.0%; Score 3034; DB 12; Length 569; Best Local Similarity 100.0%; Pred. No. 1.5e-290; Matches 569; Conservative 0; Mismatches 0; Indels 0; 00,0,2 ALIGNMENTS NUMBER OF SEQ ID NOS: 30 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 18 LENGTH: 569 ORGANISM: Homo sapiens US-09-832-161-18 TYPE: PRT à 셤 ò

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US-10-038-010-8
Squence 8, Application US/10038010
Squence 9, Application US/10038010
Squence 9, Application US/10038010
Squence 9, Application No. US20030040089A1
GENERAL INFORMATION:
JAPLICANT: HYBIGENICS
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
TITLE OF INVENTION: Protein-protein interactions in adipocyte cells
CURRENT FILING DATE: 2002-07-23
FRIOR APPLICATION NUMBER: US 60/259,377
FRIOR PILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.1
RVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII
                                                                                               QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK
                                                                                                                                              QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK
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100.0%; Pred. No. 1.5e-290;
rative 0; Mismatches 0; Indels 0;
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LOCATION: (1)..(569)

CHER INPORMATION:
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location No. US20020123082A1
Location No. US.
Location No. Methods To Identify Compounds USEFUL FOR THE TREATMENT OF
LE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF
REFERENCE: 5314-030-939
REFERENCE: 5314-030-939
RETING DATE: 2002-01-07
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                                                                                                                                                                                         181 RVTSDGMLWKKLJERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKII 240
                                                                                                                                                                                                                                                                                                                                                    301 RILIGHTESVLCLOYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMM: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 VTCSKDRSIAVWDMASPTDITLERVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC 420
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61 STAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVEHL 120
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                                                                                               RILIGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMM
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Local Similarity 100.
1es 569; Conservative
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NGTH: 569
PE: PRT
3ANISM: Homo sapiens
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                                                                                                                           272 CLKVLTGHTGSVLCLQYDERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFSNG 331
                            212 IIQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISGLRDNSIKIWDKTSLE
                                                                                                                                                                                                                                           332 LMYTCSKDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWSTS
                                                                                                                                                                                                                                                                                                                 TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                           452 DNKRIVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHD
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239 ILQDIBTIBSNWRCGRHSLORIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLE
                                                                                                  299 CKRILIGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNG
                                                                                                                                                                                                          359 MMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTS
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US-10-023-530-2

US-10-023-530-2

Sequence 2, Application US/10023530

Publication No. US20030007956A1

GENERAL INFORMATION;

APPLICANT: LEGRALIN, Pierre

APPLICANT: BLOY, Guillaume

APPLICANT: LEGRALIN, PROTEINS THAT INTERACT WITH BETA TrCP

TITLE OF INVENTION: PROTEINS THAT INTERACT WITH BETA TrCP

FILE REPERENCE: B471AA

CURRENT APPLICATION NUMBER: US/10/023,530

CURRENT FILING DATE: 2002-04-22

PRIOR APPLICATION NUMBER: G0/256,276

PRIOR PILIAGE DATE: 2000-12-18

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin version 3.1

LENGTH: 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DITLINDFLNDPAAQAEPPRSPSRTYTYISR 569
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LOCATION: (1). (219)
COTHER INFORMATION: F-box protein
US-10-023-530-2
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                            241 QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK 300
                                                                                                                              301 RILIGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLWTLIHHCEAVLHLRFNNGMM 360
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                                                                                                                                                                                                                                        EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN 480
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QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK 300
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action to us20030166587A1

but INFORMATION:
ICANT: Manning, Anthony M.
ICANT: Marcurio, Frank
ICANT: Marcurio, Frank
ICANT: Barbai, Ada
ICANT: Arcon, Arraham
E OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
E OF INVENTION: NE-MB
E OF INVENTION: NE-MB
E OF INVENTION NUMBER: US/09/832,161
ENT APPLICATION NUMBER: 09/210,060
2 RILING DATE: 1998-12-10
2 APPLICATION NUMBER: 09/210,060
2 RILING DATE: 1998-12-10
3 APPLICATION NUMBER: 09/210,060
3 RILING DATE: 1998-12-10
3 APPLICATION NUMBER: 09/210,060
3 RILING DATE: 1998-12-10
3 APPLICATION NUMBER: NO/210,060
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                                                                                                     RILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGWM
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79.0%; Pred. No. 2e-226;
tive 48; Mismatches 41; Indels 31;
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YLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIE 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 FMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTK 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----- 42
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B. OF INVENTION: Nucleic Acids, Proteins, and Antibodies

REFERENCE: PT2062-08-16

BNT FILING DATE: 2002-08-16

R APPLICATION NUMBER: 10/116,016

R FILING DATE: 2001-01/116,016

R FILING DATE: 2001-01/116,016

R APPLICATION NUMBER: 60/179,065

R RILING DATE: 2001-01-31

R APPLICATION NUMBER: 60/180,628

R APPLICATION NUMBER: 60/180,628

R APPLICATION NUMBER: 60/119,065

R FILING DATE: 2000-02-04

R APPLICATION NUMBER: 60/119,487

R FILING DATE: 2000-01-11

R APPLICATION NUMBER: 60/220,963

R APPLICATION NUMBER: 60/220,963

R APPLICATION NUMBER: 60/220,963

R APPLICATION NUMBER: 60/220,963

R RILING DATE: 2000-07-16

R APPLICATION NUMBER: 60/220,963

R RILING DATE: 2000-07-16

R R RILING DATE: 2000-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.6%; Score 989.5; DB 9; Length 265; 68.9%; Pred. No. 4.1e-89; Live 24; Mismatches 21; Indels 39
                                                                                                                                                ALL INPORMATION:
JICANT: Rosen et al.
JICANT: Rosen et al.
ROSEN ENTROPMENTION: Nucleic Acids, Proteins, and Antibodies
REFERENCE: PIZ209
RETERENCE: PIZ209
RENT FILING DATE: 2001-01-17
RENT FILING DATE: 2001-01-17
RENT FILING DATE: 2001-02-17
RENT FILING DATE: 2001-03-17
RENT OF SEQ ID NOS: 53
RENT OF SEQ ID NOS: 53
RENT OF SEQ ID NOS: 53
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                                                                          ance 30, Application US/09764848 t No. US20020077270A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 68.9
les 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SANISM: Homo sapiens 764-848-30
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764-848-30
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PRIOR PRICATION NUMBER: 60/218, 290
PRIOR PLING DATE: 2000-0144
PRIOR PLING DATE: 2000-08-12
PRIOR PLING DATE: 2000-08-14
PRIOR PPLICATION NUMBER: 60/224,518
PRIOR PPLICATION NUMBER: 60/229,344
PRIOR PPLICATION NUMBER: 60/229,344
PRIOR PPLICATION NUMBER: 60/229,344
PRIOR PPLICATION NUMBER: 60/229,345
PRIOR PPLICATION
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us-09-601-168b-2.rapb

LING DATE: 2000-11-1,
PELICATION NUMBER: 60/249,213 FILING DATE: 2000-09-29 APPLICATION NUMBER: 60/236,802 FILING DATE: 2000-10-02 APPLICATION NUMBER: 60/237,037 FILING DATE: 2000-10-02 APPLICATION NUMBER: 60/237,040 FILING DATE: 2000-10-02 FILING DATE: 2000-10-02
APPLICATION WINBER: 60/240,960
FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/239,935 APPLICATION NUMBER: 60/239,937 FILING DATE: 2000-10-13 APPLICATION NUMBER: 60/241,787 APPLICATION NUMBER: 60/246,532 APPLICATION NUMBER: 60/249,216 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,210 FILING DATE: 2000-11-17 FILING DATE: 2000-08-22 APPLICATION NUMBER: 60/225,759 PLICATION NUMBER: 60/225,213 LING DATE: 2000-08-14 APPLICATION NUMBER: 60/227,182 PLICATION NUMBER: 60/225,214 PLICATION NUMBER: 60/235,836 APPLICATION NUMBER: 60/230,438 PLICATION NUMBER: 60/215,135 LING DATE: 2000-06-30 PLICATION NUMBER: 60/225,266 APPLICATION NUMBER: 60/249,218 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,208 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,212 FILING DATE: 2000-11-17 FILING DATE: 2000-11-17 APPLICATION NUMBER: 60/249,245 LING DATE: 2000-11-17 PLICATION NUMBER: 60/249,244 APPLICATION NUMBER: 60/249,215 APPLICATION NUMBER: 60/249,264 APPLICATION NUMBER: 60/249,214 APPLICATION NUMBER: 60/249,297 APPLICATION NUMBER: 60/232,400 CATION NUMBER: 60/231,242 APPLICATION NUMBER: 60/226,681 PLICATION NUMBER: 60/249,207 APPLICATION NUMBER: 60/249,217 APPLICATION NUMBER: 60/249,211 2000-11-08 000-08-22 2000-08-14 2000-08-14 2000-10-13 000-08-14 2000-09-06 000-11-17 2-60-000 LING DATE: LING DATE: LING DATE:

43 ISNGTSSVIVSRKRPSEGNYQKEKDLCIXYFDQWSESDQVEFVEHLISRMCHYQHGHINS 102 15 FMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTK 74 75 LANGTSSMIVPKORKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINS 135 YLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIE 195 RMVRTDSLWRGLABRRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGR RWVRTDPLWKGLSERRGWDQYLFKNRPTDG--PPNSFYRSLYPKIIQDIETIESNWRCGR 103 YLKPMLQRDFITALPEQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLIE 32.6%; Score 989.5; DB 12; Length 265; 68.9%; Pred. No. 4.1e-89; tive 24; Mismatches 21; Indels 39; APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILLE REFERENCE: PIZORGI
CURRENT APPLICATION NUMBER: US/10/116,016
CURRENT FILING DATE: 2002-04-05
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
LENGTH: 265 255 HSLQRIHCRSETSKGVYCLQYDDQKIVSGL 284 221 HNLQRIQCRSENSKGVYCLQYDDEKIISGL 20 FONTSVMEDONEDESPK----KNTLWO PRIOR APPLICATION NUMBER: 60/23, 080
PRIOR FILING DATE: 2000-09-08
PRIOR PLING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/233, 064
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232, 397
PRIOR PRILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232, 401
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-10-20
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PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20 OR APPLICATION NUMBER: 60/233,064
OR FILING DATE: 2000-09-14
OR APPLICATION NUMBER: 60/233,063
OR APPLICATION NUMBER: 60/232,397
NR PILING DATE: 2000-09-14
NR APPLICATION NUMBER: 60/232,397 Sequence 30, Application US/10116016 Publication No. US20030054379A1 GENERAL INFORMATION: Query Match
Best Local Similarity 68.9
Matches 186; Conservative ; ORGANISM: Homo sapiens US-10-116-016-30 US-10-116-016-30 TYPE: PRT g qq g 9 ò ò ò ò

DB 15; Length 265;

32.6%; Score 989.5;

Query Match

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112 288 TIKIWDKNILECKRILIGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHC 347 321 TLKVWSAVIGKCLRTLVGHIGGVWSSQMRDNIIISGSTDRTLKVWNABIGBCIHTLYGHT 380 381 STVRCMHLHEKRVVSGSRDATLRVWDIETGQCL---HVLMGHVAAVRCVQYDGRRVVSGA 437 GDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLE 467 438 YDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLT 497 498 GHQSLTSGMELKDNILVSGNADSTVKIWDIKTG------QCLQTLQGPNKHQSAVTC 548 288 TIKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHC 347 348 EAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSAS 407 US-09-328-877A-21

Sequence 21, Application US/09328877A

Sequence 21, Application US/09328877A

Sequence 21, Application US/09328877A

Sequence 21, Application US/09328877A

Sequence 21, Application:

APPLICANT: Useralized Sequence Sequ 468 GHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLV---EHSGRVFR 53 MEQKLISEBDLNEMESLGDLTMEQKLISEBDLNSMKRKLDHGSEVRSFSLGKKPCKVSEY 64 MKTENCV-----AKTKLANGTSSMIVPKQRKLSASYEKEKEL--CVKYFEQWSESD 113 TSTIGLVPCSATPTIFGDLRAANGQG-----QORRRITSVQPPIGLOEWLKMFQSWSGPE 113 QVEFVEHLISOMCHYOHGHINSYLKPMLORDFITALPARGLDHIAENILSYLDAKSLCAA 168 KLLALDELIDSCEPTQVKHMQVIEPQFQRDFISLLP----KELALYVLSFLEPKDLLQA ELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAE----RRGWGQYLFKNKPPDGNAP 224 AQTCRYWRILAEDNLLWREKCKE------EGIDEPLHIKRRK-----VIKPGFIHSP PNSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDN 8 LQEKALKFMNSSEREDCNNGEPPRKIIPEK--NSLRQ--TYNSCARLCLNQETVCLASTA 6 myc tagged Query Match 21.2%; Score 644.5; DB 10; Length 626; Best Local Similarity 30.1%; Pred. No. 1.8e-54; Matches 169; Conservative 103; Mismatches 222; Indels 67; ) OTHER INFORMATION: Description of Artificial Sequence: , OTHER INFORMATION: homo sapien US-09-328-877A-21

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) ORGANISM: Homo sapiens
US-09-213-888-10
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US-09-213-888-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKD 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      427 NGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSG 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 INSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 RSIAVWDWASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTL 426
                                          437
                                                                                                        438 YDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLT 497
                                                                                                                                                                                                             GHOSLTSCMELKDNILVSGNADSTVKIWDIKTG------QCLQTLQGPNKHQSAVTC 548
348 BAVLHLRFINIGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSAS 407
                                                                                                                                                                     GHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLV---EHSGRVFR 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 KLANGTSSMIVPKQRKLSASYEKEKEL--CVKYFEQWSESDQVEFVEHLISQMCHYQHGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAANGOG-----QQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 LIERMVRIDSLWRGLAE----RRGWGOYLFKOKFPDGONAPPNSFYRALYPKIIQDIETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            314 ATLRVWDIETGOCL -- HVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHTL
                        4 KLDHGSEVRSFSLGKKPCKV----SEYTSTTGL----VPCSA----TPTTFGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 KFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKT
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                                                                                   GDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      JICANT: Gurney, Mark E.
JICANT: Li, Jinhe
JICANT: Li, Jinhe
JICANT: Pauley, Adele M.
JICANT: Pharmacia & Upjohn Company
JICANT: PAPERICATION: Bancode Them
REPERBROE: 6142
CENT APPLICATION NUMBER: US/09/213,888A
ENT FILING DATE: 1998-12-17
WARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72; Gaps
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Local Similarity 30.8%; Pred. No. 4.1e-54;
es 167; Conservative 92; Mismatches 211; Indels 7
                                                                                                                                                                                                                                                        525 LOFDEFQIVSSSHDDTILIWD 545
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LQFNKNFVITSSDDGTVKLWD 569
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ANISM: Homo sapiens
13-888-7
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426
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371 QGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSG 430
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                                                                                                                                                                                 LICANT: Gurney, Mark E.
LICANT: Balley, John
LICANT: Pauley, Adele M.
LICANT: Pauley, Adele M.
LICANT: Pharmacia & Upjohn Company
LICANT: Pharmacia & Upjohn Company
LICANT: Pharmacia & Upjohn Company
LICANTION: Human Sel-10 Polypeptides and Polynucleotides that
REFERENCE: GLOSS Them
REFERENCE: 6199-06-09
REFERENCE: 1999-06-09
REFERENCE: 1999-06-09
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                                                                                                                             ence 7, Application US/09328877A nt No. US20020177187A1
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SANISM: Homo sapiens
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      Sequence 10, Application US/09328877A

Sequence 10, Application US/09328877A

Sequence 10, US20020177187A1

SEQUENCAL INFORMATION:

APPLICANT: Gurney, Mark E.

APPLICANT: Pauley, Adele M.

APPLICANT: Pauley, Adele M.

APPLICANT: Pauley, Adele M.

TITLE OF INVENTION: Human Sel-10 Polypeptides and Polymucleotides that

TITLE OF INVENTION: Encode Them

TITLE OF INVENTION: Human Sel-10 Polypeptides

CURRENT APPLICATION NUMBER: US/09/328,877A

CURRENT FILING DATE: 1999-06-09

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.0

SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 30.8%; Pred. No. 4.1e-54;
Matches 167; Conservative 92; Mismatches 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 14, Application US/10245618; Publication No. US20030143582A1; GRNERAL INFORMATION: APPLICANT: Reed, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           544 WD 545
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-09-328-877A-10
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US-10-245-618-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 BSNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGH 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 TGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKD 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 TGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMLHEKRVVSGSRD 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367 RSIAVWDMASPIDITLRRVLVGHRAAVNVVDPDDKXIVSASGDRIIKVWNTSTCBFVRTL 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427 NGHKRGIACLOYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSG 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 LIERMVRTDSLWRGLAE-----RRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIBTI 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 KFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNGETVCLASTAMKTENCVAKT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 KLANGISSMIVPKORKLSASYEKEKEL--CVKYFEQWSESDQVEFVEHLISQMCHYQHGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 KCKE------EGIDEPLHIKRK-----VIKPGFIHSPWKSAY-----IRQ--HRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 21.1%; Score 640; DB 12; Length 540; Local Similarity 30.8%; Pred. No. 4.1e-54; nes 167; Conservative 92; Mismatches 211; Indels 7
LICANT: Strobmajer, Heimo
LICANT: Spruck, Charles
LICANT: Sangfelt, Ole
LICANT: Sangfelt, Ole
LE OF INVENTION: HCDO:
RENT PAPLICATION: HCDO:
RENT APPLICATION NUMBER: US/10/245,618
RENT APPLICATION NUMBER: US 60/404,116
OR FILING DATE: 2002-09-16
OR PILING DATE: 2002-09-15
OR PILING DATE: 2001-09-14
BER OF SEQ ID NOS: 48
ETANS: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATURE:
HER INFORMATION: Synthesized
245-618-14
                                                                                                                                                                                                                                                                                                                                                                                                                ID NO 14
NGTH: 540
PE: PRT
GANISM: Artificial Seguence
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completed: October 22, 2003, 10:34:58 e : 74 secs

482 WD 483

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18 SSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLAN 77
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
US-08-190-802A-30
Sequence 30. Application US/08190802A
Sequence 30. Application US/08190802A
Setent No. 551903
GENERAL IRFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: Whe-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STAILS: USA

ZIP: 94306-0850

ZIP: 94306-0850

COUNDUTER READRABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PLOPPY disk
COMPUTER: PLOPPY disk
COMPUTER: PLOPPY DATE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-194
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELEFAX: (415) 324-0860
INFORMATION: (415) 324-0860
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acids
TYPE: amino acids
US-08-473-089-52
US-08-487-072A-52
US-08-198-582-6
US-08-198-582-5
US-08-199-802A-62
US-08-199-802A-62
US-08-477-346-62
US-08-477-346-62
US-08-477-089-62
US-08-477-072A-62
US-09-092-508-2
US-09-092-508-2
US-09-092-508-2
US-09-092-508-16
US-09-032-508-16
US-09-032-508-16
US-09-032-508-16
US-09-032-518-16
US-09-032-518-16
US-08-646-715-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRIGINAL SOURCE:

INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13

VS.-08-190-802A-30
                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dehlinger & Associates STREET: P.O. Box 60850 CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
      HYPOTHETICAL: 1
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Best Local Simi
Matches 487;
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                                                                                                                                      October 22, 2003, 10:21:24 ; Search time 30 Seconds (without alignments) 802.496 Million cell updates/sec
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Sequence 51,
Sequence 51,
Sequence 51,
Sequence 6, A
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Sequence 30,
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Sequence 3
Sequence 3
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
                        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-477-346-30
US-08-477-089-30
US-08-177-165A-30
US-08-195-78-2
US-08-190-802A-32
US-08-477-346-32
US-08-477-346-32
US-08-477-346-32
US-08-477-346-32
US-08-177-165A-29
US-08-961-71-165A-29
US-08-961-71-9
US-08-961-716-9
US-08-971-999-6
US-08-971-999-6
US-08-477-346-66
US-08-477-346-55
US-08-477-346-55
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US-08-477-346-55
US-08-477-346-55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'ccessing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                       ein - protein search, using sw model.
                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                              1 MDPAEAVLQEKALKFMNSSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                        DB seq length: 0
DB seq length: 200000000
                                                                                                                                                                                                                       US-09-601-168B-2
3034
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Match Length DB
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2582.5
2582.5
2582.5
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520
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ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
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APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Per; TITLE OF INVENTION: Thereof; NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ž
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     SEQUENCE CHARACTERISTICS:
LENGTH: 517 amino acids
TYPE: amino acid
                                                     TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                         Best Local Similaríty
Matches 487; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-08-473-089-30
                                                                                                                                                                  US-08-477-346-30
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                                                                                       GTSSMIVPKQRKLSANYBKEKELCVKYFEQWSECDQVBFVEHLISRMCHYQHGHINTYLK 102
                                                                                                                                                                                                          257
                                                                                                                                                                                                                                                                                                               282
                                                                                                                                                                                                                                                                                                                                                 RVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASP 377
                                                                                                                                                                                                                                                                                                                                                                        437
                                                                                                                                                                                                                                                                                                                                                                                                                                                              401
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                        -TKLAN 42
                                                                                                                                                    TDITLRNULVGHRAAVNVVDFDDKYIVSASGDRTIKVMNTSTCEFVRTLNGHKRGIACLQ
                                                         GTSSMIVPKORKLSASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLK
                                                                                                                                 PMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMV
                                                                                                                                                                                                    RIDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSL
                                                                                                                                                                                                                                                                           QRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE
                                                                                                                                                                                                                                                                                                                                                                                                                      TDITLRRVLVGHRAAVNVVDFDDXYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRPDNKRIVSGAYDGKIKVWDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIDSLWRGLAERRGWGQYLFKNKPPDGKIPPNSFYRALYPKIIQDIETIESNWRCGRHSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDP 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              462 VAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFOIVSSSHDDTILIMDFLNDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nce 30, Application US/08477346
t No. 626203
RAL INFORMATION
PLICANT: Mochly-Rosen, Daria
PLICANT: Ron, Dorit
TLE OF INVENTION: Wb-40 - Derived Peptides and Uses
TLE OF INVENTION: Thereof
RRESPONDENCE: 265
RRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Mortison & Foerster
STRET: 2000 Pennsylvania Avenue, NW
STRET: 2000 Pennsylvania Avenue, NW
STATE: DC
COUNTRY: USA
COUNTRY: USA
MEDIW TYPE: Floppy disk
MEDIW TYPE: Floppy disk
MEDIW TYPE: Floppy disk
MEDIW TYPE: Ploppy disk
MEDIW TYPE: NOW, Wersion #1.25
SOFTWARE: PatentIn Release #1.0, Version #1.25
RRENT APPLICATION DATA:
APPLICATION: 514
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOSEPH CALLON: 314

APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-20N-1995
FORNEY'S AGENT: 10FORMATION:
VAME: MURASHIGE, KATE H.
SEGISTRATION NUMBER: 25.9.959
EFERENCE, POCKET NUMBER: 25.0-0025.20
LECOMMUNICATION INFORMATION:
FILE PROMES: (20.2) 887-1500
FILE PROMES: (20.2) 887-1500
FILE PROMES: (20.2) 887-0503
AMATION FOR SEQ ID NO: 30:
                        ASEREDCNRDEPPRKIITEKNTLRO
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77-346-30
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                                                                                                                                18 SSEREDCHNGEPPRKIIPEKNSIRQTYNSCARLCINQETVCLASTAMKTENCVAKTKLAN
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                                                                           Gaps
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85.1%; Score 2582.5; DB 3; Length 517; ilarity 91.4%; Pred. No. 3.1e-266; Conservative 7; Mismatches 8; Indels 31:
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                                                                                                                                                                         STREET: 2000 Pennsylvania Avenue,
CITY: Washington
STATE: DC
CCUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
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AUDKESSE:
AUDKESSE:
AUDKESSE:
AUTHORNS AND A FOGESCE
STREET: 2000 Fennsylvania Avenue, NW
STREET: 2000 Fennsylvania Avenue, NW
CITY: Washington
STATE: 00
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INPORMATION:
NAME: WURDASHIGE, KATE H.
REGISTRATION NUMBER: 250-0025.20
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-1503
INPORMATION FOR SEQ ID NO: 30:
SEQUINCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 ASEREDCNRDEPPRKIITEKNTLRQ------
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                                                                              Morrison & Foerster
  TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 517 amino acids
amino acid
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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Best Local Similarity
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ORIGINAL SOURCE
                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-487-072A-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 402 YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL
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Local Similarity 91.4%; Pred. No. 3.1e-266;
es 487; Conservative 7; Mismatches 8; Indels 31;
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87-072A-30
mce 30, Application US/08487072A
t No. 6423684
RAL INFORMATION:
PLICANT: Mochly.
PLICANT: Ron, Dorit
TLE OF INVENTION: WD-40 - Derived Peptides and Uses
     Patentin Release #1.0, Version #1.25
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US/08/473,089

07-JUN-1995

LORNEY/AGENT INFORMATION:
MAME: WITCASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REPERENCE/DOCKET NUMBER: 250-0025.22
RECOMMUNICATION NUMBER: 250-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPAX: (202) 887-1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGINAL SOURCE:
INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
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                                                                                                         18 SSEREDCHNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAKTKLAN
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                                                          Gaps
                                                          31;
85.1%; Score 2582.5; DB 4; Length 517; 91.4%; Pred. No. 3.1e-266; Live 7; Mismatches 8; Indels 31;
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498 VAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDP

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----CVKYFEQWSESDQVE 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE--RVIITGSSDSTVRV 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 OIHDDVLVTGSDDNTLKVWCIDKGEVMYTLVGHTGGVWTSQISQCGRYIVSGSTDRTVKV 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 WDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRA 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 FVEHLISOMCHYOHGHINSYLKPMLORDFITALPARGLDHIAENILSYLDAKSLCAAELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 CKEWYRVTSDGMLWKKL-IERMV------RTDSLWRGLAERRGWGQYLFKNKPPDGNAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 CDLNVHRFLKLOKFGDIFERAADKSRYLRADKIEKNWNANPIMGSAV-LRGHEDHVITCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.1%; Score 520; DB 3; Length 587; 28.8%; Pred. No. 3e-46; Artive 78; Mismatches 222; Indels 7
                                                                                                                                                                                                                                                                                                                                         ADDRESSE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIF: 10036 Avenue of the Americas
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/NG-DOS
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,578
FILING DATE: 24-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/53200/JPW/AKC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 KTKLANGTSSMI------VPKQRK--LSASYEKELL
                                  Sequence 2, Application US/08899578;
Patent No. 6087153
GENERAL INFORMATION:
APPLICANT: Greenwald, Iva
APPLICANT: Hubbard, E. Jane
TITLE OF INVENTION: SEL-10 AND USES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 28.8°
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-899-578-2
               US-08-899-578-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 --HCRIQEFKGHMDGVLTLQFNYRLLFTGSYDSTIGIWDLFTGKLIRRLSGHSDGVKTLY 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             466 VQKİIPLIIKDVENLATDNISDGSSPQDDPIMTDGADESDIPSNEQETVLDENIPYPIHL 525
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526 LSCGLDNTIKLWDVKTGKCIRTQFGHVEGVWDIAADNFRIISGSHDGSIKVWDLQSG--- 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 NSNDKIRKL-------ILDGILSTSCFPQLSYISSLVTHMIKIDFISILP-- 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 GLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERR- 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- PPDGNAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQ 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIHCRSETSK----GVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQ 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375 ASPIDITLERVLVGHRAAVNVVDFDDKYI--VSASGDRTIKVWNTSTCEFVRTLNGH--- 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 ASYEKEKELCVKYFEQWSESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPAR 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 PNCGWGLPLLHMKRARIQQNSTGSSSNADIQTQTTRPWKVIYRERFKVESNWRKG---- 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 YDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDM 374
                                                                                                                                                                                                                                                                                               JUGNIT: Tyers, Mike
JICANT: Willems, Andrew
JICANT: Willems, Andrew
JICANT: Willems, Andrew
JEOR INVENTION: METHADDS AND COMPOSITIONS FOR MODULATING UBIQUITIN
JEOF INVENTION: DEPENDENT PROTECLYSIS
3 REFERENCE: 11757.10UGUI
SENT APPLICATION NUMBER: US/09/177,165A
SENT FILING DATE: 1998-07-10
NR APPLICATION NUMBER: 60/092,443
NR APPLICATION NUMBER: 60/063,254
NR APPLICATION NUMBER: 60/063,254
NR PILING DATE: 1997-10-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 IPEKNSLROTYNSCARLCIN-QETVCLASTAMKTENCVAK-TKLANGTSSMIVPKQRKLS
462 VAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDP
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                                                                                                                                                                                       ence 30, Application US/09177165A
nt No. 6426205
RAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT SANISM: Saccharomyces cerevisiae 177-165A-30
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177-165A-30
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Gaps

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589 SMDTTIRIWDLENIWNNGECSYATNSASPCAKILGAMYTLQGHTALVGLLRLSDKFLVSA 648
                                                                                                               336 TGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV 395
                                                                                                                                                          396 VDFDD----KYIVSASGDRTIKVWNT-----------STCE----FVRTLNG 428
                                                                                                                                                                                                                                                                                                 429 HKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN--KRIVSG 486
                                                                                                                                                                                                                                                                                                                                                                                        487 AYDGKIKVWDL------VAALDPRAPAGTL--CLRTLVEHSGRVFRLQFDEFQIVSS 535
                       277 DOKIVSGLRDNTIKIWDKNTLECKRILJGHTGSVLCLOYDE-RVIITGSSDSTVRVWDVN 335
                                                                392 DNYVITGADDKMİRVYDSINKKFILQLSGHDGGVWALKYAHGGILVSGSTDRTVRVWDIK 451
                                                                                                                                                                                                                                               469 LDIVEYKNIKYIVTGSRDNTLHVWKLPKESSVPDHGEEHDYPLVFHTPEENPYFVGVLRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Doriv
TITLE OF INVENUION: WD-40 - Derived Peptides and Uses
TITLE OF INVENUION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UGA
ZIP: 2006-1812
COMPUTER READBLE FORM:
MEDIUM TYPE: FORM:
COMPUTER: IBM PC compatible
OBPRATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION UMBER: 08/487,072
APPLICATION UMBER: 08/487,072
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
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STREET: 2000 Pennsylvania Avenue,
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 32, Application US/08477346 Patent No. 6262023 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: MURASHIGE, KATE H.
REGISTRATION UNUMBER: 29,950-
REFERENCE/DOCKET NUMBER: 2550-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPRA: (202) 887-0501
INPORMATION POR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 779 amino acids
amino acid
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      649 AADGSIRGWD-AND-
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INDIVIDUAL ISOLATE:
US-08-477-346-32
                                                                                                                                                            452 KG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 TVCLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYBKEK-----ELCVKYFEQW 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 APPNSFYRALYPKIIQD-----IET--IESNWRCGRHSLQRIHCRSETSKGVYCLQYD 276
.450 NTIRLWDI----ECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAP 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 NSINLKLSQKÝPKLSQODRLRLSFLENIFÍLKÁMYNPKFVPQKTTLÄGHMTSVITČLŐFE 391
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                                          440 TSIRVWDFTRPEGQECVALLQGHTSLTSGMQLRGNILVSCNADSHVRVWDI-
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                                                                                                                                                                                                                       90-802A-32
Ince 32, Application US/08190802A
t No. 551903
RAL INFORMATION:
PLICANT: Mochly-Rosen, Daria
PLICANT: Ron, Dorit
TLE OF INVENTION: Thereof
MEER OF SEQUENCES: 265
ADDRESSEE: Dehlinger & Associates
STREET: P.O. BOX 60850
CITY: Palo Alto
                                                                                          507 AGTLCLRTLVEHSGRVFRLQ-FDEFQIVSSSHDDTILIWD 545
                                                                                                                                  EGT-CVHMLSGHRSAITSLQWFGRNMVATSSDDGTVKLWD 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin DATA:
APPLICATION NUMBER: US/08/190,802A
PILING DATE: 01-FEB-1994
CLASSIFICATION: 530
TORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 IINSLGVSQNWNKIIRKSTSLWKKLLISENFV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94306-0850
MPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-
LECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0960
TELEPRATION FOR SEQ ID NO: 32:
QUENCE CHARACTERISTICS:
LENGTH: 779 amino acids
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IGINAL SOURCE:
INDIVIDUAL ISOLATE:
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                                                                                                                                                                                          245 ----NLLFRLVANMDRSELSDLGTLIKDNLKRDLITSLPF----EISLKIFNYLQFED
                                                                              56 TVCLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEK------BLCVKYFEQW
                                                                                                                      194 TTPLAKTTKTINN-----NNIADLIESKDSIISPEYLSDEIFSAINNNLPHAYFK--
                                                                                                                                                                                                                                           169 LCAAELVCKEWYR-VTSDGMLWKKLI--ERMVRTDSLWRGLAERRGWGQYLFKNKPPDGN
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13.2%; Score 399; DB 3; Length 779;
24.3%; Pred. No. 3.8e-33;
cive 80; Mismatches 196; Indels 156; Gaps
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73-089-32
Application US/08473089
t No. 6342368
RAL INFORMATION:
PLICANT: Mochly-Rosen, Daria
PLICANT: Ron, Dorit
TILE OF INVENTION: WD-40 - Derived Peptides and Uses
MBER OF SEQUENCES: 265
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RRENT APPLICATION DATA:
**PPLICATION NUMBER: US/08/473,089
**ILING DATE: 0-JUN-1995
**ILING DATE: 0-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             536 SHDDTILIWDFLNDPAAQAEPPRSPSRTYTY 566
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APUTER READABLE FORM:
ABDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
DPERATING SYSTEM: PC-DOS/MS-DOS
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                     Local Similarity 24.3
es 139; Conservative
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168
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APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
NUMBER OF SEQUENCES: 265
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Best Local Similarity 24.3
Matches 139; Conservative
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                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
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  589 SMDTTIRIWDLENIWNNGECSYATNSASPCAKILGAMYTLQGHTALVGLLRLSDKFLVSA 648
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                                                                                                                                                                                                                                                                                        APPLICANT: Tyers, Mike
APPLICANT: Tyers, Mike
APPLICANT: Tyers, Mike
APPLICANT: Willems, Andrew
TITLE OF INVENTION: DEPENDENT PROTECLYSIS
FILE REPERENCE: 11757.10USU1
CURRENT APPLICATION NUMBER: US/09/177,165A
CURRENT APPLICATION NUMBER: US/09/177,165A
PRIOR FILING DATE: 1998-07-10
PRIOR FILING DATE: 1998-07-10
PRIOR FILING DATE: 1998-07-10
PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATCHIN VET: 2.1
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                                                   536 SHDDTILIWDFLNDPAAQAEPPRSPSRTYTY 566
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                                                                                                                                                                                                                        Sequence 29, Application US/09177165A Patent No. 6426205
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                                                                                               649 AADGSIRGWD-AND
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                                                                                                                                                                                              US-09-177-165A-29
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LENGTH: 779
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392 DNYVITGADDKMIRVYDSINKKFLLQLSGHDGGVWALKYAHGGILVSGSTDRTVRVWDIK 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              336 TGEMLNTLIHHCEAVLHLRFNNGMMYTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            452 KG-----HVFEGHNSTVRC 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----STCE----FVRTLNG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN--KRIVSG 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              487 AYDGKIKVWDL-----VAALDPRAPAGTL--CLRTLVEHSGRVFRLQFDEFQIVSS 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 -----NLLFRLVANMDRSELSDLGTLIKDNLKRDLITSLPF----EISLKIFNYLQFED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 NSINIKISQKYPKLSQQDRLRISFLENIFILKNWYNPKFVPQRTTLRGHMTSVITCLQFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 TVCLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEK------ELCVKYFEQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 TTPLAKTTKTINN-----NNNIADLIESKDSIISPEYLSDEIFSAINNNLPHAYFK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 SESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match
Local Similarity 24.3%; Pred. No. 3.8e-33;
es 139; Conservative 80; Mismatches 196; Indels 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGINAL SOURCE:
INDIVIDUAL ISOLATE: CDC4 / CDC20 protein, Fig. 15
87-072A-32
                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
NRRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 IINSLGVSQNWNKIIRKSTSLWKKLLISENFV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2550-0025.20
                                                                                                                                                                                                                                                                                                               FILING DATE: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIPICATION: 514
TORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERNCE/DOCKET NUMBER: 2550-0025.26
LECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-1500
WHATION FOR SEQ ID NO: 32:
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                                                2000 Pennsylvania Avenue, NW
                            Foerster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 779 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LECULE TYPE: protein POTHETICAL: NO TI-SENSE: NO
                                                                                                                                           ZIP: 20006-1812
MPUTER READABLE FORM:
MEDIUM TYPE: Floppy
RRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
                                                                  CITY: Washington
STATE: DC
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TLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF -- DNKR 482
                                                                                                                                                                                                                            305 GHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCS 364
                                                                                                           365 KDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVR 424
                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ADACHI, HIDEKI
APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: ANOUG, KEIZO
APPLICANT: ANAL, HIROYUKI
TITLE OF INVENTION: OXIDIZED PHOPHOLIPID DEGRADING ENZYME
TITLE OF INVENTION: AND GENE THEREOF
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & ADDRESSEE: NEUSTADT, P.C. STREET: 1755 S. Jefferson Davis Highway, Suite 400 CITY: Arlington STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 03-AUG-1994
CLASSIFICATION NUMBER: US/08/283,917
FILING DATE: 03-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07-20943/1993
FILING DATE: 03-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5849557man F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 229-030-0
TELECOMMUNICATION INUMBER: 229-030-0
TELECOMMUNICATION INUMBER: 229-030-0
TELECOMMUNICATION INUMBER: 239-030-0
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08283917
Patent No. 5849557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (703) 413-220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                              409 amino acids
                                                                                                                                                                                                                                                                                      483 IVSGAYDGKIKVW 495
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ORIGINAL SOURCE:
ORGANISM: Bos taurus
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Matches 87; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DNL 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----- ONMECV-- 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 LKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLASTAMKTENCVAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345 LIFPDTSERDNNNNNNNNNNNNNNNNNNNNNNNNNNNNNSSISKSLVEISSGSKERNDRDSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 TK---LANGISSMIVPKORKLSASYEKEK-ELCVKYPROWSESDOVEFVEHLISOMCHYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.9%; Score 392; DB 4; Length 732;
24.1%; Pred. No. 1.9e-32;
tive 84; Mismatches 172; Indels 118;
                                                                                                                                                                                                                                            (EF-2 KINASE)
                                                                                                                                                                                                                                                                                                         ORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esg.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 RRENT APPLICATION DATA: APPLICATION NUMBER: US/08/914,999
                                                                                                                                                                        PELICANT: Kyazanov, Alexey G.
PPLICANT: Hait, William N.
PPLICANT: Pavur, Karen S.
ILLE OF INVENTION: ELONGATION FACTOR-2 KINASE
ITLE OF INVENTION: AND METHODS OF USE THEREFOR
MRER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----YDYKS----
  ---- YSRKFSY 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-078
LECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                       ence B, Application US/08914999
tt No. 6346406

    Floppy disk
    IBM PC compatible

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RMATION FOR SEQ ID NO: 8:
QUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           732 amino acids
649 AADGSIRGWD-AND---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 24.19 es 119, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COPOLOGY: linear
LECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                        ERAL INFORMATION:
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ORGANISM: Dic
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Sequence 9, Application US/08283917
Patent No. 5849557
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APPLICANT: ADACHI, HIDEKI
APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: INOUE, KRIZO
APPLICANT: ARAI, HIROYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE:
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280 IVSGLRDNTIKIMDKNTLECKRILTGHTGSVLCLQYDE--RVIITGSSDSTVRVWDVNTG 337
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                                                                                                                                                                                                                                                                                               299 ETKKSGKPGPFLLSGSRDKTIKOMDVSTGMCLMTLVGHDNWVRGVLFHSGGKFLLSCADD 358
                                                 122 MVSASEDATIKVWDYETGDFERTLKGHTDSVQDISFDHSGKLLASCSADMTIKLWDFQGF 181
                                                                                                                                                                                                                                                                                                                                                       490 GKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEF--QIVSSSHDDTILIWD 545
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---KNKRCMKTLNAHEHFVTSLDFHKTAPYVVTGSVDQTVKVWE 407
                                                                                                                                                                                                         338 EMLNTLIHHCEAVLHLRF--NNGMWYTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV
                                                                                                                                                                                 396 V--DFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDR------
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PPLICANT: TSUJINOTO, MASAFUNI
PPLICANT: INOUE, KEIZO
PPLICANT: ATAI, HIROYUKI
ITLE OF INVENTION: OXIDIZED PHOPHOLIPID DEGRADING ENZYME
ITLE OF INVENTION: AND GENE THEREOF
MARRES OF SEQUENCES: 31
PRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: OBLOW, SPIVAK, MCCLELLAND, MAIER & ADDRESSEE: NEUSTADT, P.C. STREET: 1755 S. Jefferson Davis Highway, Suite 400 STATE: virginia
STATE: virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
ARRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,716
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Oblon, No. 5880272man F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 2292-030-0
LIECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3200
TELERX: (703) 413-220
TELERX: 248855 OPAT UR
PRATION FOR SEQ ID NO: 3:
OURNCE CHARACTERISTICS:
LENGTH: 409 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
LOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,917
FILING DATE: 03-AUG-1994
APPLICATION NUMBER: UP 209943/1993
FILING DATE: 03-AUG-1993
FILING DATE: 03-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ence 3, Application US/08961716 to No. 5880272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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280 IVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDE--RVIITGSSDSTVRVWDVNTG 337
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                                                                     Gaps
Query Match 11.7%; Score 354; DB 2; Length 409; Best Local Similarity 29.2%; Pred. No. 8e-29; Matches 87; Conservative 57; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: OXIDIZED PHOPHOLIPID DEGRADING BNZYME TITLE OF INVENTION: AND GENE THEREOF NUMBER OF SEQUENCES: 31 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 209943/1993
FILING DATE: 03-AUG-193
ATTORNEY/AGENT INPORMATION:
NAME: Oblon, No. 5849557man F.
REGISTRATION NUMBER: 24,618
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,917
FILING DATE: N3-MG-1994
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                                                                                                                                           338 EMLNTLIHHCEAVLHLRF--NNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNV 395
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360 KTLRVWDY------KNYRCMKTLNAHEHFVTSLDFHKTAPYVVTGSVDQTVKVWE 408
y Match 11.7%; Score 354; DB 2; Length 410; Local Similarity 29.2%; Pred. No. 8.1e-29; hes 87; Conservative 57; Mismatches 110; Indels 44; Gaps
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completed: October 22, 2003, 10:26:37 me : 32 secs

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SEQUENCE FROM N.A.
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Q8chd5 mus musculu
Q923h0 mus musculu
044382 drosophila
Q97de3 drosophila
Q9754 heterodera
Q922c7 mus musculu
Q92xf4 drosophila
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                                                        October 22, 2003, 10:14:07; Search time 104 Seconds (without alignments) 1411.845 Million cell updates/sec
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                                                                                                                1 MDPAEAVLQEKALKFMNSSE........PAAQAEPPRSPSRTYTYISR 569
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Og6ri2 1
Og61e0 1
Og6a16 1
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                              830525 segs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
                                      using sw model
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Q9Z159
Q9R167
Q8RV90
Q8CHD5
Q9CHD5
Q9VDE3
Q9VDE3
Q9BJ54
Q9BJ54
Q9BJ77
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1: sp_archea:*

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5: sp_invertebrate:*

6: sp_mammal:*

7: sp_marchea:*
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## ALIGNMENTS

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"Ubiquitin ligase Skpl/Cul 1/F-box protein FWD1.",
Proc. Natl. Acad. Sci. U.S.A. 96:3859-3863(1999).
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MEDLINE-99075339; PubMed=9859996;
Yazon A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M.,
Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.;
"Identification of the receptor component of the IkappaSalpha-
                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mamalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2002 (TrEMBLrel. 22, Last annotation update)
Ubiquitin ligase FWD1 (Beta-transducin repeat containing protein)
(F-box-WD40 repeat protein 1).
BTRC OR FEXW1.
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99199275; PubMed=10097128;
Hatakeyama S., Kitagawa M., Nakayama K., Shirane M., Matsumoto M.
Hattori K., Higashi H., Nakano H., Okumura K., Onoe K., Good R.A.
Nakayama K.-1:;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the EMBL/GenBank/DDBJ databases.
569 AA.
PRT;
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MEDLINE=21601157; PubMed=11735228;
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PRELIMINARY;
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Submitted (FEB-2001)
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SEQUENCE FROM N.A.
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       KRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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SMART; SM00256; FBOX; 1.

SMART; SM00250; WD40; 4.

PROSITE; PS50101; FBOX; 1.

PROSITE; PS50082; WD_REPEATS_1; 6.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS50094; WD_REPEATS_REGION; 1.

Repeat; WD_repeat.

SEQUENCE 569 AA; 65047 MW; BC7C7A44815BED96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=99145465; PubMed=9990853;
Spencer E., Jiang J., Chen Z.J.;
Signal.induced ubiquitination of IkappaBalpha by the Slimb/beta-TrCP.";
                                                                                                                                                                                                                                                                                                                       01-NAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 98.5%; Score 2990; DB 11;
Best Local Similarity 98.4%; Pred. No. 3.8e-248;
Matches 560; Conservative 3; Mismatches 6;
                                                                                                   ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                                                                                                  iliwdflndpahaepprspsrtytysk 569
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BTRC.
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ENBL, AF112979; AAD04181.1; -
NGJ, NGJ:1338871; Btrc.
InterPro; IPR001810; F-box.
InterPro; IPR00180; WD40.
Fram; PF00446; F-box; 1.
Fram; PF00446; WD40; 7.
PRINTS; PR00120; GPROTEINBRPT.
ProDom, NATORO 18; WD40; 4.
                                                                                                                                                                                                                                                                             PRELIMINARY;
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STRAIN-C57BL/6J; TISSUE-Thymus;

STRAIN-C57BL/6J; TISSUE-Thymus;

The FANTOM Consortium.

The FANTOM Consortium.

The RIKEN Genome Exploration Research Group Phase I & II Team;

The RIKEN Genome Exploration Research Group Phase I & II Team;

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Sciurognathi, Muridae, Murinae, Mus.
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
F-box(WD-repeat protein 1B.
Wus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae
(11)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
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                                                                                                                                                                                                                                                                                                                            KRIVSGAYDGKIKWMDLVAALDPRAPAGTLCLRTLVBHSGRVFRLQFDEFQIVSSSHDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHITENILSYLDAKSLCAABLVCKEWY
                                         VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC
                                                                                          VICSKDRSIAVWDMASPIDIILRRVLVGHRAAVNVVDFDDKYIVSASGDRIIKVWNTSTC
                                                                                                                                                                                    EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN
                                                                                                                                                                                                                              KRIVSGAYDGKIKVWDLMAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDT
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Local Similarity 97.9%; Pred. No. 4.1e-247;
es 557; Conservative 4; Mismatches 8; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QUENCE FROM N.A.

nston J., Elledge S.J., Harper J.W.;

bmitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

BL, AFI10396, AAD41025.1; -.

D, MGI:1338871; Btrc.

terPro; IPRO10181; P-box.

terPro; IPRO10181; P-box.

terPro; IPRO10181; P-box.

am; PF00468; P-box; J.

am; PF00460; W440; J.

INTS; PR00320; GPROTEINBRPT.

ODON; PD000018; WD40; 4.

ART; SM00256; FBOX; 1.

ART; SM00256; FBOX; 1.

OSITE; PSS0181; FBOX; 1.

OSITE; PSS0181; FBOX; 1.

OSITE; PSS0082; WD REPEATS_1; 6.

OSITE; PSS0082; WD REPEATS_RGION; 1.

OSITE; PSS0082; WD REPEATS_RGION; 1.

OSITE; PSS0294; WD_REPEATS_REGION; 1.

PPAT; WD repeat.

QUENCE 569 AA; 65209 MW; E6DDCAD28D551D9D CRC64;
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-OCT-2002 (TrEMBLrel. 22, Last annotation update)
ta-transducin repeat-containing protein.
RC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
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-MAY-2000 (TrEMBLrel. 13,
-OCT-2002 (TrEMBLrel. 22,
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                                                                                                                                                                                                                                                         468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197 RRGWDQYLFKORPTDG--PPNSFYRSLYPKIIQDIETIESNWRCGRHNLQRIQCRSENSK 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Brain;
Okazaki N., Kikuno R., Ohara R., Inamoto S., Hara Y., Nagase T.,
Ohara O., Koga H.;
Prediction of the coding sequences of mouse homologues of KIAA gene:
I. The complete nucleotide sequences of 100 mouse KIAA-homologous
cDAAs identified by screening of terminal sequences of cDNA clones
supplied from size-fractionated libraries. ";
Submitted (CT-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 PARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAE
                             223 NSFYRSLYPKLIQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDDKIISGLRDNS
                                                                                                                    IKIWDKSSLECLKVLTGHTGSVLCLQYDERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNE
                                                                                                                                                                                                  AVLHIRFSNGLMVTCSKDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASG
                                                                                                                                                                                                                                                                                                                                                                     29 PPRKIIPEKNSIRQTYNSCARLCINQETVCLASTAMKTENCVAKTKLANGTSSMIVPKOR
                                                                                         IKIWDKNTLECKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCE
                                                                                                                                                                         349 AVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASG
                                                                                                                                                                                                                                                         DRIIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEG
                                                                                                                                                                                                                                                                                                  DRIIKVWSTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIBCGACLRVLEG
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      NSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNT
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
VCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFQIISSSHDDTILIWDFLNVPPSAQNETRSPSRTYTYISR 563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
MKIAA0696 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                               EFQIVSSSHDDTILIWDFLNDPAAQAEPPRSPSRTYTYISR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.8%; Score 2360; DB 1:81.9%; Pred. No. 5e-194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 443; Conservative 38; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Best Local 9
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                                                                     420
                                                                                                                                                       480
                                                                                                                                                                                             440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 VRCLQNTSVMEDQNEDESPKKSALWQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYFDQW 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SESDOVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 SESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALPEQCLDHIAENILSYLDARS 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPP 228
                             320
                                                                                                             380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDPAEAVLQEKALKFMNSSERE---DCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQ--E 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VICSKDRSIAVWDMASAIDIILLRRVLVGHRAAVNVVDFDDKYIVSASGDRIIKVWSTSTC
                                                                                                                                                       EFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN
                                                                                                                                                                                                                                        KRIVSGAYDGKIKWWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLOFDEFQIVSSSHDDT
                                                                     VTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
mmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
BI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rausberger R.;

rausberger R.;

bmitted (JUL_2002) to the EMBL/GenBank/DDBJ databases.

BL; BC034261, AAH34261.1;

terPro; IPR001810; F-box.

terPro; IPR001810; F-box.

am; PF000464; F-box.

am; PF000464; F-box.

INTS; PR00320; GPROTEINBRPT.

OBOTH: PR000018; WD40; 4.

URT; SM00256; FBOX; 1.

GRITE; PS50081; WD REPEATS 1; 5.

OSITE; PS50082; WD REPEATS 2; 7.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K022 PRELIMINARY; PRT; 563 AA.
K7022,
-OCT-2002 (TrEMBLrel. 22, Created)
-OCT-2002 (TrEMBLrel. 22, Last sequence update)
-NAR-2003 (TrEMBLrel. 23, Last annotation update)
box and WD-40 domain protein 1B.
s musculus (Mouse).
                                                                                                                                                                                                                                                                                                                          ILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                                                                                                                                                                                                                                                                                                es 454; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSUE=Kidney;
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IKIWDKNTLECKRILIGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCE 348
                                                                                                                                                                                                                                                                                        349 AVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                          463 HEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRLQFD 522
                                                                                                                                                                                                                                                                                                                                                                                                                                   HEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFD 528
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                                                                                                                                                                                                                                                                                                                                                                                SESDQVEFVEHLISRMCHYQHGHINSYLKFMLQRDFITALPEQGLDHIAENILSYLDARS
                                                                                         LCAAELVCKEWQRVISEGMLWKKLIERMVRTDPLWKGLSERRGWDQYLFKNRPTDG--PP
                                                                                                                                           NSFYRALYPKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNT
                                                                                                                                                                    283 IKIMDKSSLECLKVLTGHTGSVLCLQYDERVIVTGSSDSTVRVMDVNTGBVLNTLIHHNE
                                                                                                                                                                                                                                                                                                                          343 AVLHLRFSNGLMVTCSKDRSIAVWDMAPCHRYHFTPCSGWPRAAVNVVDFDDKYIVSASG
SESDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKS
                                                                      LCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPP
                                                                                                                                                                                                                                                                                                                                                               DRIIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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MEDLINE=98121115; PubMed=9461217;
Jiang J., Strubl G.;
"Regulation of the Hedgehog and Wingless signalling pathways by the box/Wp40-repeat protein Slimb.";
Nature 391:493-496(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Erachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

NCBI_TaxID=7227,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS06678; WD_REPEATS_1; S.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
REPEAT; WJ PEPEAT: SEQUENCE 510 AA; 58952 MW; DBB0243D3730A5E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFQIVSSSHDDTILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           044382;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
SLIMB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFQ11SSSHDDT1LIWDF1NVPPSAQNETRSFFRTYTYISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.9%; Score 2089.5; DB 5; 78.3%; Pred. No. 7.7e-171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF032878; AAC38852.1; -. FlyBase; FBGn0024423; slmb. InterPro; IPR001680; F-box. InterPro; IPR001680; Wb40. Pfam; PF00646; F-box; 1. Pfam; PF00400; Wb40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS, PRO0320, GPROTEINBRPT.
ProDom; PD000018; WD40; 4.
SMARI; SM00256; FBOX; 1.
SMARI; SM00320; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local S
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                                                                                                                             448
                    314
                                                     388
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                                                                                                                                                                                                                                                                         VRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRRVLVG
                                                                                                                                                  HRAAVNVVDFDDKYIVSASGDRTIKVWSISTCEFVRTLNGHKRGIACLQYRDRLVVSGSS
                                                                                                                                                                                                                                 DNTIRLWDIBCGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAFAS
                                                       VRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKDRSIAVWDMASPTDITLRRVLVG
                                                                                                                             HRAAVMVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSS
                                                                                                                                                                                                    DNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDPRAPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ls musculus (Mouse).
Karyota, Metažoa; Chordata; Craniata; Vertebrata; Euteleostomi;
mmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
pI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atia N., Herter J.R., Slaga T.J., Fuchs S.Y., Spiegelman V.S.; ouse homolog of HOS (mHOS) is overexpressed in skin tumors and plicated in constitutive activation of NF-kappaB."; Dinited (JUN-201) to the EMBL/GenBank/DDBJ databases.

Bi, AYO38079; AAK72055.1; -.

D; MGI:2144023; Fbxwlb.

terPro; IPR001810; F-box.
terpro; IPR00180; WD40.
am; PF00460; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.3%; Score 2286; DB 11; Length 563; 75.7%; Pred. No. 1.2e-187; 1.ve 46; Mismatches 65; Indels 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                563 AA; 64741 MW; 9AB562F3FF5E3496 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -DEC-2001 (TrEMBLrel. 19, Created)
-DEC-2001 (TrEMBLrel. 19, Last sequence update)
-MAR-2003 (TrEMBLrel. 23, Last annotation update)
box/WD40 repeat-containing protein HOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               563 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTS; PR00320; GPROTEINBRPT.
ODOM; PD000018; WD40; 4.
IART; SM00220; WD40; 7.
IART; SM00220; WD40; 7.
OSITE; PS50018; PBOX; 1.
OSITE; PS50082; WD REPEATS_1; 5.
OSITE; PS50082; WD REPEATS_2; 7.
OSITE; PS50082; WD REPEATS_2; 7.
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QUENCE 563 AA;
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RAINEBERKELEY,
DINE=20196006; PubMed=10731132;
ams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
amatides P.G., Scherer S.E., Holt R.W., Hoskins R.A., Galle R.F.,
orge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
tton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
andon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.
n.K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.
ril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
llew R.W., Basu A., Baxendale J., Bayaktaroglu L., Beasley E.M.,
eson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
rkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
rits K.C., Busam D.A., Baxter H.C., Cadieu E., Center A., Chandra I.,
erry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
dson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
thin K.J., Evangelista C.C., Ferriera S., Fleischmann W.,
sler C., Gabzrelian A.E., Garg N.S., Gelbart W.M., Glasser K.,
odek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               418
                                                                                                                                                                                                                                                          179 WYRVTSDGMLWKKLIERMVRTDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPK 238
                                                                                                                                                                                                                                                                                                                                                                                     IIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLE 298
                                                                                                                                                                                                                                                                                                                                                                                                                          361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHD 538
MKTENCVAKTKLANG---TSSMIVPKQRKLSAS--YEKEKELCVKYFEQWSESDQVEFVE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVKTLMGHTGSVLCLQYDDKVIISGSSDSTVRVWDVNTGEMVNTLIHHCEAVLHLRFNNG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DTKRIVSGAYDGKIKVWDLVAALDPRAASNTLCLNTLVEHTGRVFRLQFDEFQIVSSSHD 481
                                                          62
                                                                                                                                                                CKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKY1VSASGDRTIKVWNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAVICSKDRSIAVWDMISPSEITLRRVLVGHRAAVNVVDFDEKYIVSASGDRIIKVWSTS
                                                                                                                           HLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCAAELVCKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCEFVRTLNGHKRGIACLOYRDRLVVSGSSDNSIRLWDIECGACLRVLEGHEELVRCIRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              osophila melanogaster (Fruit fly).
Raryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
optera; Bradopterrygota; Diptera; Brachycera; Muscomorpha;
hydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VDE3;
-MAY-2000 (TrEMBLrel. 13, Created)
-MAY-2000 (TrEMBLrel. 13, Last sequence update)
-MAR-2003 (TrEMBLrel. 23, Last annotation update)
MB protein (SLIMB) (LD086699).
MB OR CG3412.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          510 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTILIWDFLNDPAAQAEPPRSPS 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DTILIWDFLNFTPNENKTGRTPS 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OUENCE FROM N.A.
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BI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                     239
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                                                             4,
                                                                                                                           119
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178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 WYRVISDGMLWKKLIERMVRIDSLWRGLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 METDKIMDETN-SNAQAFITTMLYDPVRKKDSSPTYQTERELCFQYFTQWSESGQVDFVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 HLISOMCHYOHGHINSYLKPMLORDFITALPARGLDHIAENILSYLDAKSLCAAELVCKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 WLRVISEGMLWKKLIERKVRTDSLWRGLAERRNWMQYLFKPRPGQ-TQRPHSFHRELFPK
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-Ovary, and Imaginal disks;
MIDLINE-202529; PubMed=10781936;
Miletich I., Limbourg-Bouchon B.;
"Drosophila null slimb clones transiently deregulate Hedgehog-independent transcription of wingless in all limb discs, and induce decepentablegic transcription linked to imaginal disc regeneration.";
Mech. Dev. 93:15-26(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Berkeley; Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Erise E., George M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celliker S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.9%; Score 2089.5; DB 5; Length 78.3%; Pred. No. 7.7e-171; Live 49; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AEC03733; AAF55813; -.
EMBL, AF222924; AAF632141; -.
EMBL, AF222923; AAF63213.1; -.
EMBL, AY118898; AAM50758.1; -.
EMBL, AXII8898; AAM50758.1; -.
ENBL, AXII8808; AAM50758.1; -.
InterPro; IFR001810; F-box.
InterPro; IPR001810; F-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat; WD repeat. _____S8952 MW; F4D5DF126F58A012 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0320; GPROTEINBRPT.
PRODOM; ED000118; WD40; 4.
PROSITE; PS50181; FBOX; 1.
PROSITE; PS500678; WD REPEATS 1; 5.
PROSITE; PS50082; WD REPEATS 2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00646; F-box; 1.
Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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318 RVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMAVTCSKDRSIAVWDMASP 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TDITLERVLVGHRAAVNVVDFDDXXIVSASGDETIKVWSTSTCEFVETLNGHKEGIACLQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 YRDRLVVSGSSDNTIRLMDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 QAALDPRAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFLNVPPSAQNET 240
                                                                                                                                                                               RFDSKRIVSGAYDGKIMIWDLAAALDPMTPPNSICIKTLSQHTGRVFRLQFDEFQIISSS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              438 YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498 VAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDPAAQAEPP
378 TDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTSTCEFVRTLNGHKRGIACLQ
                                                                                                      241 ASTCEFVRTLNGHKRGIACLQYRDRLIVSGSSDYSIRLWDIECGNCLRVLEGHEELVRCI
                                                                                                                                               RFDNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.5%; Score 1230; DB 11; Length 252; 92.9%; Pred. No. 1.9e-97; Live 7; Mismatches 11; Indels 0
                                                                                                                                                                                                                                                   ---- CAEPPRSPS 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC008552; AAH08552.1; -.
                                                                                                                                                                                                                                                                                                                                                                                        Q922C7;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to f-box and WD-40 domain protein 1B (Fragment)
FBXW1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 AA; 28424 MW; F71737CBD7A9F75F CRC64;
                                                                                                                                                                                                                                                                                                                                                                         252 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS, PRO0320; GPROTEINBRPT.
ProDom; PD000018; WD40; 3.
SWART; SW00320; WD40; 3.
PROSITE; PS00678; WD REPEATS_1; 5.
PROSITE; PS50082; WD REPEATS_2; 6.
PROSITE; PS50294; WD REPEATS_2; 6.
                                                                                                                                                                                                                              HDDTILIMDFLN-DPAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:2144023; Fbxwlb.
InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 234; Conserv
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NON_TER 1
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SEQUENCE FROM N.A.
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                                                                                                                                                                                     301
                                                                                                                                                                                                                              537
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                                                                                                                                                                                                                                                                      361
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                                                                                                                                                                                                                                                                                                                                                                      Q922C7
                                                                                                                                                                                                                                                                                                                                RESULT 11
0922C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 IBRMVRTDSLWRGLAERRGWGQYLFKNK-------PPDGGNAP---PNSFYRALY 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 PKIIQDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNT 296
                       239 IIQDIBTIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLE 298
                                                                                                                                               301
                                                                                                                                                                                                                              361
                                                                                                                                                                                                                                                                                                                                                                           DTKRIVSGAYDGKIKVWDLVAALDPRAASNTLCLNTLVEHTGRVFRLQFDEFQIVSSSHD 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                 CKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNG
                                                                                                                                CVKTLMGHTGSVLCLQYDDKVIISGSSDSTVRVWDVNTGEMVNTLIHHCEAVLHLRFNNG
                                                                                                                                                                                                          MMVICSKDRSIAVWDMTSPSEITLRRVLVGHRAAVNVVDFDEKYIVSASGDRIIKVWSTS
                                                                                                                                                                                                                                                                                            SCEFVRILNGHKRGIACLQYRDRLVVSGSSDNSIRLWDIECGACLRVLEGHEELVRCIRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IERQVRNDALWAGLAIRRGWKKYFFCSKDQATRAISQSWRQPKNGEDALEFQHKFYRELY
                                                                                                                                                                                       MMVTCSKDRSIAVWDMASPTDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWNTS
                                                                                                                                                                                                                                                                      TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF
                                                                                                                                                                                                                                                                                                                                                   DNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -JUN-2001 (TrEMBLrel. 17, Created)
-JUN-2001 (TrEMBLrel. 17, Last sequence update)
-JOCT-2002 (TrEMBLrel. 22, Last annotation update)
ta-transducin repeat-containing protein (Fragment).
terodera glycines (Soybean cyst nematode).
karyota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; lenchoidea; Heteroderidae; Heteroderinae; Heterodera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QUENCE FROM N.A.

valeva E.S., Yakovlev A.G., Masler B.P.;

lant parasitic nematode b-TRCP.";

bmitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

BL; AF339101; AAK26376.1; -..

EL; AF339101; AAK26376.1; -..

terPro; IPR001680; W040.

am; PF00400; W040; 7.

INTS; PR00320; GPROTEINBRPT.

oDom; PD000018; WD40; 7.

ART; SM00320; WD40; 7.

OSITE; PS00303; WD REPEATS_1; 6.

OSITE; PS00394; WD REPEATS_2; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          430 AA; 47916 MW; 4ABC3FF2DFE3A50B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49.4%; Score 1498; DB 5; 69.9%; Pred. No. 4e-120; ative 36; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DILLIMDFLNFTPNENKTGRTPS 504
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es 283; Conservative
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N TER 1
QUENCE 430 AA;
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497

437

QUENCE FROM N.A. RAIN-Berkeley;

apleton M., Brokstein P., Hong L., Agbayani A., Carlson J., ampe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., nzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., noo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K. C., Lewis S.E., Rubin G.M., Celniker S., benited (OCT-2001) to the BMBL/GenBank/DDBJ databases.

apleton M., Brokstein P., Hong L., Agbayani A., Carlson J., ampe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., orge R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., randa A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., tel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Iniker S.; RAIN-Berkeley

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EMBL; AE003480; AAG22246.1; -.
EMBL; AY061300; AAL68231.1; -.
EMBL; AY075401; AAL68231.1; -.
FlyBase; FBD0041171; ago.
Interpro; IPR001810; F-box. 1326 AA; 141360 MW; 3F42C873CFA3027F CRC64; 516 V---EHSGRVFRLOFDEFQIVSSSHDDTILIWD 954 RDGNMPPIASPWKAAYMR--QHI--IEMNWR-PROSITE; PS50181; FBOX; 1.
PROSITE; PS00678; WD\_REPEATS\_1; 5.
PROSITE; PS50082; WD\_REPEATS\_2; 7.
PROSITE; PS50294; WD\_REPEATS\_REGION; 1.
REPEAT; MD\_rEPEATS\_REGION; 1.
SEQUENCE 1326 AA; 141360 MW; 3F42C8 PRINTS, PR00320; GPROTEINBRPT. ProDom; PD000018; WD40; 2. SMART; SM00256; FBOX; 1. SMART; SM00320; WD40; 7. Pfam; PF00646; F-box; 1, Pfam; PF00400; WD40; 7. Conservative Query Match Best Local Similarity Matches 158; Conserv В qq a ò ВЪ d g ö В ò ò  $\delta$ ò  $\delta$ 

01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ11071. 1232 SGPNKHHSAVTCLOFNSRFVVTSSDDGTVKLWD 1264 PRELIMINARY; O9NUX6; 9XUN60 RESULT 13

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butelé Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo Homo sapiens (Human) NCBI\_TaxID=9606; ACCOCCOS NATIONAL NAT

SEQUENCE FROM N.A. IISSUB=Placenta; Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

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427 NGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSG 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 KLANGISSMIVPKORKLSASYEKEKEL -- CVKYFEQWSESDOVEFVEHLISQMCHYQHGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 RAANGQG-----QORRRITSVQPPTGLQEWLKMPQSWSGPEKLLALDELIDSCEPTQVKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 INSYLKPMLORDFITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 LIERMVRTDSLWRGLAE-----RRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 ESNWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRILTGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 TGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNGMMVTCSKD
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                                                   Euteleostomi;
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                                Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Cararrhini, Hominidae, Homo,
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                 Koepp D.M., Winston J.T., Harper J.W., Elledge S.J.; Submitted (MAY-2010) to the EMBL/GenBank/DDBJ databases. EMBL; AF38178; AAK60269.1; -. InterPro; IPR001810; F-box. InterPro; IPR001680; WD40. Pfam; PF00666; F-box, 1. PF00466; P-box, 1. PF00460; WD40.
                                                                                                                                                                                                            S.J., Harper
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 21.1%; Score 640; DB 4; L. Best Local Similarity 30.8%; Pred. No. 3.1e-46; Matches 167; Conservative 92; Mismatches 211;
                                                                                                                       [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. Winston J.T., Koepp D.M., Zhu C., Elledge & "A family of mammalian F-box proteins."; Curr. Biol. 9:1180-1182(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00256; FBOX; 1.

SMART; SM00320; WD40; 8.

PROSITE; PS50181, PBOX; 1.

PROSITE; PS0062; WD_REPEATS 1; 5.

PROSITE; PS0062; WD_REPEATS 2; 7.

PROSITE; PS0294; WD_REPEATS 2; 7.

REPEAT: MD repeat.

NON TER

SEQUENCE 561 AA; 63165 MW; BBICCIEZ200
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ProDom; PD000018; WD40; 2.
                        Homo sapiens (Human)
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shikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Y.,
Atsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
Akamura Y., Nagahari K., Masuho Y., Saito K., Yamamoto J., Wakamatsu A.,
Abunitara Y., Nagahari K., Masuho Y., Sasaki N.;
Amuso human cDNA sequencing project.";
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Amuso J., Ako1933: BAA91986.1;
Arcologis Ako1986.1;
Arcologis Ako1986.1;
Arcologis Ako1980;
Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso J., Amuso
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-DEC-2001 (TrEMBLrel. 19, Last sequence update)
-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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1 J., Pauley A.M., Myers R.L., Shuang R., Brashler J.R., Yan R.,

1 J., Pauley A.M., M.E.;

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Patent: WO 9938969-Agrags_Aug-1999;
Patent: WO 9938969-Agrags_Aug-1999;
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PRENARANA SEISDEDOS FERNÂNDO (FR); CONCORDET JEAN PAUL (FR);
NAT SANTE RECH MED (FR); KROLL MATHIAS (FR); DURAND HERVE (FR);
PENAROUS RICHARD (FR); MARGOTTIN FLORENCE (FR); PASTEUR INSTITUT (FR)
                                                                                                                                                      Durand, H., Benarous, R.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 42 from Patent WO0075184.
AX057166
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I Chases 1 to 2151)

Benarous, R., Margottin, F., Durand, H., Seisdedos, F.A., Kroll, M. and Concordet, J.P.

CONCORDER TECP protein

L Patent: JP 2002501746-A 1722-JAN-2002,

INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE, INSTITUT PASTEUR

OS Artificial Sequence
PD 22-JAN-2002
PF 29-JAN-1999 JP 2000529429

PF 39-JAN-1999 JP 200052
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                                 AlaCysLeuArgValLeuGluGlyHisGluGluLeuValArgCysIleArgPheAspAsn
                                                                                                                                                                                     GCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTCGATTGATAAC
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           eArgLeuTrpAspIleGluCysGly
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Human beta TrCP protein.
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TITLE Direct Submission  JOURNAL Submitted (19-PEB-1999) Pathology, NYU Medical Center, 550 First  FEATURES  Location/Qualiflers  Location/Qualiflers  Location/Qualiflers  Location/Qualiflers  Location/Qualiflers  Location/Qualiflers  Location/Qualiflers  Location/Qualiflers  Location/Qualiflers  Location="How sapiens"  Aboutce="Texton:606"  Chromosome="10"  Mapp="10024"  Location="FBMIA"  /Gene="FBMIA"  /Gene="FBMIA"  /Gene="FBMIA"  /Gene="FBMIA"  /Goods = "Contains one F-box domain and seven WD40 domains;  forms an SCF with Skpl and Cull"  /Coods = "Contains one F-box domain and seven WD40 domains;  forms an SCF with Skpl and Cull"  /Coods = "Contains one F-box domain and seven WD40 domains;  forms an SCF with Skpl and Cull"  /Coods = "Contains one F-box domain and Seven WD40 domains;  forms an SCF with Skpl and Cull"  /Coods = "Contains one F-box domain and Seven WD40 domains;  forms an SCF with Skpl and Cull"  /Coods = "Contains one F-box domain and Seven WD40 domains;  forms an SCF with Skpl and Cull"  /Coods = "Contains one F-box domain and Seven WD40 domains;  forms an SCF with Skpl and Cull"  /Coods = "Contains one F-box domain and Seven WD40 domains;  forms an SCF with Skpl and Cull"  /Coods = "Contains one F-box domain and Seven WD40 domains;  forms an SCF with Skpl and Cull"  //Coods = "Contains one F-box domain and Seven WD40 domains;  forms an SCF with Skpl and Cull"  //Coods = "Contains one F-box domain and Seven WD40 domains;  ISYLDAKSICADENCHININGNUMENCRYMINGSEREDCNNGEPERSECTORY  NYOPEDDRYINGNUMENCRYMINGNUMENCRYMINGSERSINGNUMENT  ISSYLDAKSICADENCRYMINGNUMENCRY	3.75e-274 3034.00 100.00\$ 1ty: 100.00\$ 9	US-09-601-168B-2 (1-569) x AF129530 (1-2151)  QY	41 ArgGlnThrTyrAsnSerCysAlaArgLeuCysLeuAsnGlnGluThrValCysLeuAla 60  190 AGACAGACATACAACAGCTGTGCCAGACTTAAACCAAGAAACAGTTTAGCA 249  61 SerThrAlaMetLysThrGluAsnCysValAlaLysThrLysLeuAlaAsnGlyThxCsr 80  5250 AGCACTGTATGAAGACTGAGAATTGTGGCCAAAAACTTGCCAATGGCACTTCC 309  81 SerMetlleValProLysGlnArgLysLeuSerAlaSerTyrGluLysGluLysGluLeu 100  82 By AGTATGATTGTGCCCAAGGAAACTTCTCAGCCAAAAGCTTCC 309  83 SerMetlleValProLysGlnArgLysLeuSerAlaSerTyrGluLysGluLeu 100  94 AGTATGATTGTGCCCAAGCAACGGAAACTTCTCAGCAAAGGAACTG 369  95 CONTAINANT AND AGTATGAGCAACGGAAACTTCAGCAAAGGAACTT 429  96 CONTAINANT AGTATGAGCAGCAAGGAAACTTCAGCAAAAGGAACTT 429  97 TGTGTCAAATACTTTGAGCAGTCAGAACTCAGAACTTGTGGAACTTT 429  98 CONTAINANT AGTATGAGCAGTTAAACTTAAAACTTAAAACTTTG 489
11eThrGlySerSerAspSerThrValArgValTrpAspValAsnThrGlyGlumetLeu 340		541 IleLeulleTrpAspPheLeuAsnAspProAlaAlaGlnAlaGluProProArgSerPro 560 1690 ATCCTCATCTGGGACTTCCTAAATGATCCAGCTGCCCAAGCTGAACCCGCTTCCCT 1749 561 SerArgThrTyrThrTyrIleSerArg 569 1150 TCTCGAACATACACTGCGAG 1776	AF129530 2151 bp mRNA linear PRI 31-OCT-1999 Homo sapiens chromosome 10 F-box protein Fbw1A (FBW1A) mRNA, complete cds.  NA F129530 AF129530 AF129530.1 GI:6164609 Homo sapiens Homo sapiens Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Elkaryote; Metazoa; Chordata; Catarrhini; Hominidae; Homo.  I (bases 1 to 2151) Cenciarrelli, C., Chiaur, D.S., Guardavaccaro, D., Parks, W., Vidal, M. Identification of a family of human F-box proteins L Curr. Biol. 9 (20), 1177-1179 (1999) E 20003060 D 10531035 E 2 (bases 1 to 2151) S Chiaur, D.S. and Pagano, M.

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NKPPDGNAPPNSFYRALYPKIIQDIETIBSNWRCGRHSLQRIHCRSETSKGVYCLQYD
DQKIVSGLRDNTIKIWDKNTLECKRILTGHTGSVLCLQYDBRVIITGSSDSYRVWDV
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TLCLRTLVBHSGRVFRLQFDEFQIVSSSHDDTILIMDFLNDPAAQAEPPRSFSRTYYY
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LSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLI ERMVRTDSLWRGLAERRGWGQYLFK
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24 rue de Fg.St-Jacques, 75014
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Y14153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Margottin,F., Bour,S.P., Durand,H., Selig,L., Benichou,S., Richard,V., Thomas,D., Strebel,K. and Benarous,R.
A novel human WD protein, h-beta Trcp, that interacts with HIV-1 Vpu connects CD4 to the ER degradation pathway through an F-box motif
                                                                                                                 LeuAspProArgAlaProAlaGlyThrLeuCysLeuArgThrLeuValGluHisSerGly
                                                                                       521 ArgValPheArgLeuGlnPheAspGluPheGlnIleValSerSerHisAspAspThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     beta-transducin repeats; beta-TRCP gene; WD repeat.
Homo sapiens (human)
Homo sapiens
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Submitted (03-JUL-1997) R. Benarous,
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                  1390 AGGCTGGTAGTGAGTGGCTCATCTGACAACACTATCAGATTATGGGACATAGAATGTGGT
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301 ArgileLeuThrGlyHisThrGlySerValLeuCysLeuGlnTyrAspGluArgValIle 320 	IleThrGlySerSerAspSerThrValArgValTrpAspValAshThrGlyGluMetLeu 340 IleThrGlySerSerAspSerThrValArgValTrpAspValAshThrGlyGluMetLeu 340 ATAACAGGATCATCGGATTCCAGGTCAGAGTGGAATACAGGTAAAATACAGGTAAAATGCTA 108 AShThrLeuIleHisHisCysGluAlaValLeuHisLeuArgPheAshAshGlyMetMet 360	6 380   120	381 ThrleudrgargvalleuvalglyHisargAlaalavalAsnvalvalaspPheAspAsp 400 	valSeralaSerGlyAspargThrIleLysValTrpAsnThrSerThrCys 42 	AnGlyHisLysArgGlyIleAlaCysLeuGlnTyrArgAsp 44 	ArgieuValValSerGlySerSerAspAsnThrIleArgieuTrpAspIleGluCysGly 	AlacysLenArgYalLeucluCiyHisGluGlubeuValArgcysIieArgPneAspAsn 			7 7	CCC CCC CCC CCC CCC CCC CCC CCC CCC CC	561 SerangThrTyThrTyTleSerarg 569 	AP101784 18-JAN-1999 N Homo sapiens b-TRCP variant E3RS-1kappaB mRNA, partial cds.		Homo saptens Eukaryota, Metazoa, Chordata; Craniata, Vertebrata, Buteleost Eukaryota, Metazoa, Chordata; Catarrhini; Hominidae, Homo. Mammalia, Butheria, Primates, Catarrhini; Hominidae, Homo. 1 (bases 1 to 1818)	
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/rpt_unit=516544 UNT 628 a 467 c 513 g 543 t	nt Scores: 3.75e-274 Length: 2151 5.: 334.00 Matches: 569 Similarity: 100.00\$ Mismatches: 0 atch: 100.00\$ Indels: 0 Gaps: 0	88-2 (1-569) x HSBTRCP (1-2151) 1 MetAspProAlaGlublaValLeuGlnGluLySAlaLeuLySPheMetAsnSerSerGlu 20	2 70	Leuala 60        TAGCA 24	SerthralametrysThrGluasnCysValalaLysThrLysLeuAlaAsnGly	81 SerMetileValProLysGlnArgLysLeuSerAlaSerTyrGluLysGluLysGluLeu 	101 CysValLysTyrPheGludInTrpSerGluSerAspGlnValGluPheValGluHisLeu 120 	21	GIDArgAspPhelleThrAlaLeuProAlaArgGlyLeuAspHisIleAlaGluAsnile 1	61 LeuSerTyrLeuAsphlaLysSerLeuCysAlaAlaGluLeuValCysLysGluTrpTyr 18	81 ArgValThrSerAspGlyMetLeuTrpLysLysLeulleGluArgMetValArgT 	SerLeuTrpargGlyLeualaGluargargGlyTrpGlyGlnTyrLeuPheLys	221 ProproAspGlyAsnAlaProProAsnSerPheTyrArgAlaLeuTyrProLysIleIle 240	241 GlnAspileGluThrileGluSerAsnTrpArgCysGlyArgHisSerLeuGlnArgile 260 	261 HisCysArgSerGluThrSerLysGlyValTyrCysLeuGlnTyrAspAspGlnLys1le 280	281 ValserGlyLeuargaspasnThrileLysileTrpasplysashThrLeuGlucysLys 300 

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WNTSTCERPURLINGHKRGIACLQYRDRLVVGSSDNTTRLWITLUNGHRGGRVFRLGFBEE
VRCIRFDNKRLVGGAYDGRKIXWMDLVAALDPERAFTTYTISR"

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Mann, M. and Ben-Neriah, Y.
Direct Submission
Submitted (27-007-1998) Immunology, He
Medical School, Jerusalem, Israel
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGAGACAACACAATCAAGATCTGGGATAAAAACACATTGGAATGCAAGCGAATTCTCACA
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                            421 TTTGAGCAGTGGTCAGATCAAGTGGAATTTGTGGAACATCTTATATCCCAAATG
                                                                                                                      GATGGCATGCTGTGGAAGAAGCTTATCGAGAATGGTCAGGACAGACTTCTCTGTGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrileGluSerAsnTrpArgCysGlyArgHisSerLeuGlnArgIleHisCysArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluThrSerLysGlyValTyrCysLeuGlnTyrAspAspGlnLysIleValSerGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgAspAsnThrIleLys1leTrpAspLysAsnThrLeuGluCysLysArgIleLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCCATACAGGTTCAGTCCTCTCTCTCTATGATGAGAGTGATCATCATAACAGGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerAspSerThrValArgValTrpAspValAsnThrGlyGluMetLeuAsnThrLeuIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1081 TCGGATTCCACGGTCAGAGTGTGGGGATGTAAAAAAAAGGTGAAATGCTAAAACACGTTGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACCATTGTGAAGCAGTTCTGCACTTGCGTTTCAATAATGGCATGATGGTGACCTGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysaspargSerIleAlaValTrpAspMetAlaSerProThrAspIleThrLeuArgArg
                                                                                                                                                                                           IleThrAlaLeuProAlaArgGlyLeuAspHisIleAlaGluAsnIleLeuSerTyrLeu
                                                                                                                                                                                                                                                                                                                                                                        AspGlyMetLeuTrpLysLysLeuIleGluArgMetValArgThrAspSerLeuTrpArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AsnAlaProProAsnSerPheTyrArgAlaLeuTyrProLysIleIleGlnAspIleGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATGCTCCTCCCAACTCTTTTTATAGAGCACTTTATCCTAAAATTATACAAGACATTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyHisThrGlySerValLeuCysLeuGlnTyrAspGluArgValIleIleThrGlySer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HisHisCysGluAlaValLeuHisLeuArgPheAsnAsnGlyMetMetValThrCysSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ThrLeudsnGlyHisLysArgGlyIleAlaCysLeuGlnTyrArgAspArgLeuValVal
PheGluGlnTrpSerGluSerAspGlnValGluPheValGluHisLeuIleSerGlnMet
                                                                                            CysHisTyrGlnHisGlyHisIleAsnSerTyrLeuLysProMetLeuGlnArgAspPhe
                                                                                                                                                                                                                                                                                                                                      GATGCCAAATCACTATGTGCTGCTGAACTTGTGTGCCAAGGAATGGTACCGAGTGACCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyLeuAlaGluArgArgGlyTrpGlyGlnTyrLeuPheLysAsnLysProProAspGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAGATCGTTCCATTGCTGTATGGGATATGGCCTCCCCAACTGACATTACCCTCCGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValLeuValGlyHisArgAlaAlaValAsnValValAspPheAspAspLysTyrIleVal
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485 1561 505 1621 525 1681 545

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                                                                                                                                                                                                                                                                                                                                                                                                                                               QDIETIESNWRCGRHSLQRIHCRSETSKGVYCLQYDDOKIVSGLRDNTIKIWRKNTLE
CKRLLTGHTGSVLCLQYDBRVIITGSSDSYRVWDVNTGBM.NTLIHHCBAVLHLRFN
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QIVSSSHDDTILIMPELNDFAAQAEPPRSPRTYTYISR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 AGGICICIGIGGCIGGGCIGCICCAGCCIGGCGGACAGCAIGCCIICGCIGCGAIGCCIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 IleThralaLeuProAlaArgGlyLeuAspHisIleAlaGluAsnIleLeuSerTyrLeu 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 ArdGACCCGGCCGAGCCGGTGCTGCAAGAAGGCACTCAAGTTTATGTGCTCTATGCCC 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 AsnAsnGlyGluProProArgLysIleIleProGluLysAsnSerLeuArgGlnThrTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 AAGACTGAGAATTGTGTGGGCCAAAACAAACTTGCCAATGGCACTTCCAGTATGATTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProLysGlnArgLysLeuSerAlaSerTyrGluLysGluLysGluLeuCysValLysTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         398 CCCAAGGAAACGGAAACTCTCAGCAAGCTATGAAAAGGAAAAGGAACTGTGTGTCAAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 PheGluGlnTrpSerGluSerAspGlnValGluPheValGluHisLeuIleSerGlnMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    458 TTTGAGCAGTGGTCAGAGTCAGATCAAGTGGAATTTGTGGAACATCTTATATCCCAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CysHisTyrGlnHisGlyHisIleAsnSerTyrLeuLysProMetLeuGlnArgAspPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysThrGluAsnCysValAlaLysThrLysLeuAlaAsnGlyThrSerSerMetIleVal
                                                                                                                                                                                                   /codon_start=1
/product="beta-transducin repeat containing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetAspProAlaGluAlaValLeuGlnGluLysAlaLeuLysPheMet
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569
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Conservative:
Mismatches:
Indels:
                                                                                                                   Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2308 bp mRNA linear PRI 01-MAY-2002
Homo sapiens, beta-transducin repeat containing, clone MGC:40028
BC027994.
BC027994.1 GI:20380815
MGC.
                                  1501 GTGTTAGAAGGCCATGAGGAATTGGTGGTTGTATTCGATTTGATAACAAGAGAAAGTC 1560
                                                                                                                                                  AGTGGGGCCTATGATGGAAAATTAAAGTGTGGGGATCTTGTGGCTGCTTTGGACCCCCGT 1620
                                                                                                                                                                                                                                                             GCTCCTGCAGGGACACTCTGTCTACGGACCCTTCTGGAGCATTCCGGAAGAGTTTTTCGA 1680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1741 GACTICCIAAAIGAICCAGCIGCCAAGCIGAACCCCCCCCGTICCCCTICICGAACAIAC 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: nisc_mgo@nhgif.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.
Hansen,N., Ho,S.-L., Karlins,E., Laric,P., Legaspi,R., Maduro,Q.L.,
Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J.
Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C.,
Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                         CTACAGTITGATGAATTCCAGATTGTCAGTAGTTCACATGATGACACAATCCTCATCTGG 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                             524
                                                                                                                                                                                                                                                                                                                                                                                                                                          AspPheLeuAsnAspProAlaAlaGlnAlaGluProProArgSerProSerArgThrTyr 564
                                                                                                                                                                                                                                                                                                                                  LeuGlnPheAspGluPheGlnIleValSerSerSerHisAspAspThrIleLeuIleTrp 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 62 Row: e Column: 7
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4502476.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2308)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (08-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                          SerGlyAlaTyrAspGlyLysIleLysValTrpAspLeuValAlaAlaLeuAspProArg
465 ValLeuGluGlyHisGluGluLeuValArgCysIleArgPheAspAsnLysArgIleVal
                                                                                                                                                                                                                       AlaProAlaGlyThrLeuCysLeuArgThrLeuValGluHisSerGlyArgValPheArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ogapbs-remail.nih.gov
Trissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: National Institutes of Health Intramural
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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Nas musculus beta-TrCP protein E3RS-IKappaB mRNA, complete cds.
AF099932.1 GI:4008019
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Mus musculus

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota, Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (Dases 1 to 1712)

Yaron, A., Hatzubai, A., Davis, M., Lavon, I., Amit, S., Manning, A.M.,

Andersen, J.S., Mann, M., Mercurio, F. and Ben-Neriah, Y.

IkappaBalpha-ubiquitin ligase

Mature 396 (6711), 590-594 (1998)
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Yaron, A., Hatzubai, A., Mercurio, F., Manning, A.M., Andersen, J.S.,
Mann, M. and Ben-Neriah, Y.
                                                          LeuGlnPheAspGluPheGlnIleValSerSerHisAspAspThrIleLeuIleTrp
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Submitted (19-OCT-1998) Immunology, Hebrew University of
Ein Karem, Jerusalem 91120, Israel
Location/Qualifiers
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67 AGAGAAGACTGTAATAATGGCGAACCCCTAGGAAGATAATACCAGAGAAGAATTCACTT 126
                                                                                                                                                                                                                                                                                         21 ArgGluAspCysAsnAsnGlyGluProProArgLysIleIleProGluLysAsnSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 TGTGTCAAGTATTTTGAGCAGTGGTCAGAGTCTGATCAAGTGGAATTTGTAGAACACCTT
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                                                                                                                                                                                         MetAspProAlaGluAlaValLeuGlnGluLysAlaLeuLysPheMetAsnSerSerGlu
                                                                                                                                                                                                                                         7 ATGACCCGGCAGAGGCGGTGCTGCAGGAGAAGCGCTTAAGTTTATGAATTCCTCAGAG
                                                                                                                                                                                                                                                                                                                                                                                              41 ArgGlnThrTyrAsnSerCysAlaArgLeuCysLeuAsnGlnGluThrValCysLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerThrAlaMetLysThrGluAsnCysValAlaLysThrLysLeuAlaAsnGlyThrSer
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Mismatches:
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             99.12%
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Best Local Similarity:
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Contact: MGC help desk
Bmail: cgapbbe-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Blickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
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VNVVDPPDKYIVSAGGRTIKVWNTSTCEFVRTINGHKRGIACLQYRBDRLVVSGSSDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 8 Row: o. Column: 21
This clone was selected for full length sequencing because it passed the following selected for full length sequencing because it
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TLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWDFLNDPAAHAEPPRSPSRTYTY
                                                                                                                                                                                                                                 Direct Submission
Submitted (28-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
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arose spontaneously from a senescent normal mammary
(clonal) outgrowth infected with the virus MMTV."
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/lab_host="DH10B"
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Matches:
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|db_xref="LocusID:12234"
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JOURNAL Submitted (04-AUG-1998) Department of Molecular and Cellular Biology, Medical Institute of Bioregulation, Kyushu University, 3-1-1, Maedashi, Higashi-ku, Fukuoka 812-8582, Japan Location/Qualifiers source 1.2775	SG	/note="similar to beta-tra protein TrcP; P-box protein /codon_start=1 /product="ubiquitin ligase /protein id="AAD17755.1" /db_xref="GI:4336327" /bb_xref="GI:4336327" /bb_xref="GI:4336327" /ranslation="MDPABAVLQEKA NCARLCINOETVCILTSTAMKTENOV KYPEQWSESDQVEFVEHISQMCHYC LSYLDAKSICAABLVCKBWYRVTSDC NKPPDENNAFRYRYTSDC NKPPDENNAFRYRYTSDIE DQKIVGENDNITKUMDSTLODIE DQKIVGENDNITKUMDSTLECKRI NACEMLNTLIHGEAVLHIRENNGMN VNVVDFDDKYIVSASGDRTIKVWNTS TICLRTLVEHSGRAVFRLGFDEFQIVG ISR"	Algment Scores:  Alignment Scores:  Pred. No.:  Roore:  Percent Similarity:  Best Local Similarity:  Best Local Similarity:  98.59	Oy 1 MetaspproalaglualavalleuGlnGluLysalaLeuLysPheMetasnSerSerGlu 20	
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NSCARLCINGETVOLTSTAMMTERNOVAKAKLANGTSBOLMABETAKUT FERNESKYL
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TILCLRTLVEHSGRYFRLQFDEFQIVSSSHDDTILIMDFLNDFAAHAEPPRSFAFRT
                                                                                                                                                                                                                                AF112979 1710 bp mRNA linear ROD 02-MAR-1999 Nus muscullus beta-transducin repeat containing protein mRNA, complete cds. AF112979
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                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Bummalia; Butheria; Rodentia; Sciurognathi; Muridae, Murinae; Mus.

(bases 1 to 1710)
Spencer, E., Jiang, J. and Chen, Z.J.
Signal-induced ubiquitination of IkappaBalpha by the F-box protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol type="mRNA"
/db_raref="taxon:10090"
/db_raref="taxon:10090"
/function="ubiquitinates phosphorylated IkBa"
/function="beta-TrCP; F-box protein; IkB-ubiquitin ligase;
substrate recognition subunit of SCF complex; similar to
Homo sapiens beta-TrCP and Drosophila melanogaster Slimb"
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                        541 ileLeulleTrpAspPheLeuAsnAspProAlaAlaGlnAlaGluProProArgSerPro
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/protein_id="AAD04181.1"
/db_xref="GI:4140718"
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Submitted (10-DEC-1998) Molecular Biology and Oncology, UT
Southwestern Madical Ceter, 5323 Harry Hines Blvd, Dallas,
75235-9148, USA
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1 AIGGACCGGCAGGCGGTCCTGCAGSAGAAGCGCTTAAGTTTATGAATTCCTCAGAG 60 21 AAGGACCGGCAGGCGGTCCTGCAGSAGAAGCGCTTAAGTTTATGAATTCCTCAGAG 60 21 AAGGAASDCysAsnAsnGlyGluProProArgLys1leIleProGluLysAsnSerLeu 40 61 AGGACTGTAATAATGGCGAACCCCTAGGAAGATAATACCGAGGAAGAATTCCTT 120 41 ArgGlnThrTyrAsnSerCysAlaArgLeuCysLeuAsnGlnGluThrValCysLeuAla 60 121 AGGACTGCAAGCTGGCCAGGCTTTGCATAAACCAAGAGATATGTCTAACA 180 61 SerThrAlaMetLysThrGluAsnCysValalaLysThrLysLeuAlaAsnGlyThrSer 80 11	SerMetileValProbysGlnArgipsLeuSerAlaSerTyrGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluCluLysGluCluCcAgCcAgCcGAAACTCTCAGCAAGCTATGAGAAAGGAAAAAGGACTGCysValLysTyrPheGluGlnTrpSerGluSerAspGluValGluPheValGluHisLeuHll	ATAICCCAAATGTGCACAGGGCACATCAACTCCTACCTAAAACCTATGCTG  ATAICCAAAAAGTGGCACATGGGCACTCAACTCCTACCTAAAACCTATGCTG  GLAAGASPPHSILEThrAlaLeuProAlaArgGJyLeuAspHisileAlaGluAsnIle  CAGAGGGATTTCATAACTGCACCCAGCACGGGGTCTGGACCACACGCTGAGAAACTT  LeuSerTyrLeuAspAlaLysSerLeuCysAlaAlaGluLeuValCysLysGluTrpTyr	481 CTGTCATACTTGGACGCCAAGTCACTGTGCTGCTGAGCTGGTGCAAGGAATGGTAC 540  181 ArgValThrSerAspGlyMetLeuTrpLysLysLeuIleGluArgMetValArgThrAsp 200  181 ArgValThrSerAspGlyMetLeuTrpLysLysLeuIleGluArgMetValArgThrAsp 200  541 CGCGTGACGTCGGACGGCATGCTGTGCAAAAAGCTCATCGACAAGGATGCTCACGACGCAC 600  201 SerLeuTrpArgGlyLeuAlaGluArgArgGlyTrpGlyGlnTyrLeuPhelysAsnLys 220  601 TCTCTGTGACAGGCCTGAGAGACCAAGAGCAACAACAACAACAAAAAAAA	Proprokspdlysshlaproproksnserpheryrargalareutyrprolysileile	261 HisCysArgSerGluThrSerLysGlyValTyrCysLeuGlnTyrAspAspGlnLysIle 280  [11111111111111111111111111111111111	301 ArgIleLeuThrGlyHisThrGlySerValLeuCysLeuGlnTyrAspGluArgValIle 320	341 ASNThrLeulleHisHisCysGluAlaValLeuHisLeuArgPheAsnAsnGlyMetMet 360   1

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CLQYDERVIITGSSDSTVRWPNVTGEMLIYTLJHHGCAVLHLRRNGMWYTGSCRSCRSI
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            Amphibia, Batrachia, Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopodinae; Xenopodinae; Xenopodinae; Xenopodinae; Xenopous.

El (Bases 1 to 1671)

Speak, W., Keiper, B.D., Stratowa, C. and Castanon, M.J.
Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in anaphase are rescued by Xenopus cDNAs encoding N-ras or a protein with beta-transducin repeats cDNAs encoding N-ras or a protein with beta-transducin repeats (1993)

By 3130289

By 313141

Original source text: Xenopus laevis (library: S. cerevisiae expression library of X.laevis oocytes) cDNA to mRNA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mismatches:
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ocytes"
1..1671
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="beta-TrCP"
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341 c 424 g
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48. .1604
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281 ValSerGlyLeuArgAspAsnThrileLysIleTrpAspLysAsnThrLeuGluCysLys 300
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    2252
4451
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  Length:
Matches:
Conservative:
Mismatches:
Indels:
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  9.69e-21
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                                    Percent Similarity:
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Query Match:
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IVSRKRPSEGNYOKEKDLCIKYFDOWSESDOVEFVEHLISRNCHYOHGHINSYLKPWL
SOFD TTALRED BEQGLDHIARNILSYLDARSILCARALLYCKEWGRYST SEGNIWKKLIERNYR
TOPLWKGLSERRGWOOTLFKURP TOGPPNSFRSLYPKIIODIETISSNWRCHRHLO
RIQCRSENSKGYYCLQYDDEKIISGLEDNSIKIWDKTSLECLKVLTGHTGSVLCLQYD
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KIKKWNDLOGAALDPRAANNYNDFDKYTUSHSCARCHRUBERDYNLINGBERDHILIWDFLN
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AB033280
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Submitted (05-OCT-1999) Masaru Katoh, National Cancer Center,
Genetics Division; Tsukiji 5-Chome, Chuo-ku, Tokyo 104-0045, Japan
(E-mail:mkatoh@ncc.go.jp, Tel:81-3-3542-2511(ex.4402),
Fax:81-3-3541-2685)
                                                                     517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ., Sagara, N., Kirikoshi, H., Takagi, A., Miwa, T., Hirai, M.
                                                                                                            1434 GTCGCTGCTTTGGACCCCCGTGCGCCTGCAGGGACCCTGTGTCTCCGGACTCTTGTGGAG
                                                                                                                                                       HisSerGlyArgValPheArgLeuGlnPheAspGluPheGlnIleValSerSerHis
                        TTTGATAACAAGAGAATAGTCAGTGGAGCATATGACGGGAAAATTAAAGTGTGGGGACCTT
                                                                     ValAlaAlaLeuAspProArgAlaProAlaGlyThrLeuCysLeuArgThrLeuValGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Katch, M.
Molecular cloning and genomic structure of the betaTRCP2 gene
chromosome 5q35.1
AB033280.1 GI:7209810
BTRCP2; F-box and WD-repeats protein beta-TRCP2 isoform
HOmo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome 5435.1
Biochem. Biophys. Res. Commun. 269 (1), 103-109 (2000)
20160458
                                                                                                                                                                                                                                                                     1554 GAIGACACTAICCICAICIGGGAITTICICAACGACCCA 1592
                                                                                                                                                                                                                                            AspAspThrIleLeuIleTrpAspPheLeuAsnAspPro 550
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....2252
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/organism="Homo sapiens
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501 c 558 g
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/chromosome="5"
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157. .1746
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/gene="BTRCP2"
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Katoh, M.
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Koike, J

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IACLQYRDRLVVSGSSDDNTTLRNDIEGGRECLWCITSSHDDTILIMDFLN
                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 27 Row: i Column: 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 SerMetIleValProLysGlnArgLysLeuSerAlaSerTyrGluLysGluLysGluLeu 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372 AIGGAGCCC---GACTCGGTGAITGAGGACAAGACCATCGAGCTCATGAACACTTCAGIT 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            429 ATGGAAGATCAAAATGAAGATGAGTCCCCAAAG-------AAAAATACTCTT 473
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                    Tissue Procurement: Lou Staudt

CDM Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 943

Web site:

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,

R. M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetAspProAlaGluAlaValLeuGlnGluLysAlaLeuLysPheMetAsnSerSerGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 SerThrAlaMetLysThrGluAsnCysValAlaLysThrLysLeuAlaAsnGlyThrSer
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451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue type="Lymph, lymphoma"/clone_lib="NIH_MGC_85"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                          location/Qualifiers
cgapbs-r@mail.nih.gov
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Best Local Similarity:
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Homo sapiens, F-box and WD-40 domain protein 1B, clone MGC:21122
IMAGE:4419029, mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1657 ATTTTGATTTGGGATTTCTTAAATGTGCCTCCCAGTGCCCAGAATGAGACCCGTTCTCCC 1716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1417 GCCTGTTTAAGAGTCCTAGAGGGACATGAAGAATTGGTCCGATGCATCCGGTTTGATAAC 1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTGACCCTCGAGCCCCAGCAAGCACATTGTGTTTGCCACATTGGTGGAACATTCTGGA
                                                                                                                                                            AACACATTGATCCACCACAATGAGGCTGTATTGCACTTAGGCTTCAGCAATGGACTGATG 1116
                                                                                                                                                                                                                                                                             ACTITIACGCCGIGICCIGGITGGCCACCGGGCIGCCGICAAIGIAGIAGACTITGACGAC 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuAspProArgAlaProAlaGlyThrLeuCysLeuArgThrLeuValGluHisSerGly 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ArgValPheArgLeuGlnPheAspGluPheGlnIleValSerSerHisAspAspThr 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 IleLeuIleTrpAspPheLeuAsnAspProAlaAlaGlnAlaGluProProArgSerPro 560
                                                                                                             341 AsnThrLeuIleHisHisCysGluAlaValLeuHisLeuArgPheAsnAsnGlyMetMet 360
                                                                                                                                                                                                                          ValThrCysSerLysAspArgSerlleAlaValTrpAspMetAlaSerProThrAspIle 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysTyrIleValSerAlaSerGlyAspArgThrIleLysValTrpAsnThrSerThrCys 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgLeuValValSerGlySerSerAspAsnThrIleArgLeuTrpAspIleGluCysGly 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaCysLeuArgValLeuGluGlyHisGluGluLeuValArgCysIleArgPheAspAsn 480
321 IleThrGlySerSerAspSerThrValArgValTrpAspValAsnThrGlyGluMetLeu 340
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1 (bases 1 to 4395)
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Submitted (02-APR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                          GTAACTGGCTCTTCAGATTCTACGGTGAGAGTGTGGGATGTGAACACGGGTGAAGTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1297 GAATTTGTTCGTACTCTCAATGGGCACAAGCGGGGCATTGCCTGTCTCCAGTACAGGGAT
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1717 TCCAGAACATACACTTACATCTCTAGA 1743
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101 Cysvally	01 CysvallysTyrPheGl    :::        : 58 TGTATTAAATATTTTGA	21 Ileser        18 ATTTCA	4178	61 LeuSerTyrLeuAspAlaLy 	81 ArgValThrs         98 CGAGTGATCT	01 SerLeuTrpArg        :: 58 CCCTATGGAAA	21 ProProAspGlyAsnAlaB	41 GlnaspileGluThril 	61 HisCysArgSerGluThrSerLys 	81 ValSerGlybeuArgAspAsnThr :::	01 ArgileLeuThrGlyHis :::::	21 IleThrGlySerSerAspSerThr :::	41 ASDThrLeulleHisHisCys 	61 ValThrCysserLy 	81 ThrLeuArgArgValLeuVa. 	01 LystyrllevalSerAlaSer 	21 GluPheval           12 GAATTTGTT	41. Arg 72. CGC

461 AlaCysLeuArgValLeuGluGlyHisGluGluLeuValArgCysIleArgPheAspAsn 480

QQ	1632	
ò	481	LysArgileValSerGlyAlaTyrAspGlyLysIleLysValTrpAspLeuValAlaAla 500
QQ	1692	1692 AAGAGGATTGTCAGTGGGGCCTATGATGGGAAAATTAAAGTTTGGGACTTGCAAGCTGCT 1751
ò	501	501 LeuAspProArgAlaProAlaGlyThrLeuCysLeuArgThrLeuValGluHisSerGly 520
QO	1752	1752 CTTGACCCTCGAGCCCCAGCACATTGTGTTTGCGCACATTGGGAACATTCTGGA 1811
ò	521	521 ArgValPheArgLeuGlnPheAspGluPheGlnIleValSerSerSerHisAspAspThr 540
qq	1812	CGTGTGTTTCGGCTCCAGTTTGATGAGTTTCAGATCATCAGCAGCTCCCATGATGACACT 1871
δλ	541	IleLeuIleTrpAspPheLeuAspAspProAlaAlaGlnAlaGluProProArgSerPro 560
qo	1872	ATTITGATITGGGATITCTTAAAIGTGCCTCCCAGGAATGAGACCCCTTCTCCC 1931
ò	561	SerargThrTyrThrTyrIleSerarg 569
qu	1932	1932 TCCAGAACATACACTTACATCTCTAGA 1958
Search	complet	Search completed: October 22, 2003, 16:26:46

Search completed: October 22, 2003, 16:26:46 Job time : 5030 secs

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GenCore version 5.1.6
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ein - nucleic search, using frame\_plus\_p2n model

October 22, 2003, 14:49:27 ; Search time 2665 Seconds (without alignments) 5189.211 Million cell updates/sec

......PAAQAEPPRSPSRTYTYISR 569 1 MDPAEAVLQEKALKFMNSSE. Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext US-09-601-168B-2 BLOSUM62 score: table:

22781392 segs, 12152238056 residues

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45562784 umber of hits satisfying chosen parameters:

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Maximum Match 100%
Listing first 45 summaries

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- LOORGLOG - TOORGEO - THREADS=1 - XGAPOP=10 - XGAPOP=6
- TOORGHOO - TOORGEO - THREADS=1 - XGAPOP=10 - XGAPOP=6

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9D est1: \*
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em gss pln: \*
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em\_gss\_mam:.em\_gss\_mus:.em\_gss\_rod:.em\_gss\_rod:.em\_gss\_phg:.em\_gss\_vrl:.em\_gss

gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	K032221 Mus mus	15257 MUS IIIUB	81W 2521	0760 CDA46-HO	15560 AGENCOUR	1993 AL898993	30902 AGEN	14526 UI-M-FY0	4304 UI-M-EHO	4188 UI-M-EXO	9 6	7271	9860	1102 UI-N	8909	16650	0387	18002	20826	24867	20806	20.42	1690T	1220	50.00	9775	12586	.016	53637	25358 AGE	19157	2623 AL64.	1-10 COTT	100 K 000 L L	05200 AGE	102120 CZ1200	13313 01-N-100	COCCOCIA COCCO	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	M-10 (280224	345696 676407 NO	
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## ALIGNMENTS

RESULT 1 AK032221

AK012221
Mus musculus adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430504E23 product:beta-transducin repeat containing protein, full insert sequence. AK032221 AK032211 GI:26082733 HTC: CAP trapper. Mus musculus (house mouse) Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus DEFINITION ACCESSION VERSION KEYWORDS

ORGANISM

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/tissue_type="Olfactory brain"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1. .2897
Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 210-0045, Japan (E-mail:genome-resegsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Fax:81-45-503-9216)
Fax:Brary was prepared and sequenced in Mouse Cenome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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(MGD|MGI:1338871, GB|NM_009771, evidence: BLASTN, 100%,
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Please visit our web site for further details.
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Mismatches:
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/srrain="057BL/63"
/db_xref="PANTOM_DB:6430504E23"
/db_xref="taxon:10090"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                               Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes 20499374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Warahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. sequencing pipeline with 384 multicapillary sequencer General Connergence analysis (RISA) system-384-format General Res. 10 (11), 1757-1771 (2000)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

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                                            Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
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484 1SerGlyAlaTyrAspGlyLysIleLysValTrpAspLeuValAlaAlaLeuAspProAr 504  1628 GAGCGGAGCCTATGATGGGAAAATTAAAGTGTGGGATCTTATGGCTGCTTTGGACCCGCG 1687  504 GAlaProAlaGlyThrLeuCysLeuArgThrLeuValGluHisSerGlyArgValPheAr 524  1688 TGCTCCAGCAGGGACTCTGTGCGGACATTGTGGAGCATTTGGAAGATTTCCG 1747  524 GLeuGlnPheAspGluPheGlnIleValSerSerHisAspAspThrIleLeuIleTr 544  1748 CCTCCAGTTTGATGAATTGCAGATGCAGAGATTCTCGAAGAGTTTTCCG 1747  544 pAspPheLeuAsnAspProAlaAlaGlnAlaGluProProArgSerProSerArgThrTy 564  1808 GACTTCCTGAATGATCAGTGCTCACCTCAGCGCTCCCCTTCTCGGACATA 1867  554 rThrTyIlleSerArg 569  1868 CACCTACATCTCCAGA 1883	AX083257  Mus musculus adult male hippocampus CDNA, RIKEN full-length enriched library, clone:C630031K01 product:beta-transducin repeat containing protein, full insert sequence.  AX083257  AX083257.1 G1:26101148  HTC: CAP trapper.  Mus musculus (house mouse)   Carning, P. and Hayashizaki, Y. Carninci, P. and Hayashizaki, Y. High-efficiency full-length of Meth. Enzymol. 303, 19-44 (1999279253 (10349636 2 Carninci, P., Shibata, Y., Hayat Itoh, M., Konno, H., Okazaki, Y., Normalization and subtraction		Fullwake, X., Indue, X., Iogawa, Y., Idawa, M., Induaka, Y., Ishikawa, T., Ogawa, T., Data, Y., Kawa, Y., Okazaki, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 11076861		
	AK083257 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURGANISM	REFERENCE AUTHORS TOTALE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	TITLE JOURNAL MEDLINE PUBMED	AUTHORS
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124 tCysHisTyrGlnHisGlyHisIleAsnSerTyrLeuLysProMetLeuGlnArgAspPh 144  548 GTGTCACTACCAGCACATCAACTCCTACCTAAAACCTATGCTGCAGAGGATTT 607  144 elleThrAlaLeuProAlaArgGlyLeuAspHisIleAlaGluAsnIleLeuSerTyrLe 164  608 CATAACTGCACCAGCAGGGGTCTGGACCACTGCTGAGAACATTCTGTCATACTT 667  164 uAspAlaLysSerLeuCysAlaAlaGluLeuValCysLysGluTryrArgValThrSe 184  668 GGACGCAAGTCACTGTGTGCTGCTGTGTGTGTGTGTGTATTTGTCATACTT 667  184 rAspGlyMetLeuTrpLysLysLeuIleGluArgMetValArgThrAspSerLeuTrpAr 204  186 GGACGGCTGTGGAAAAGCTCATGGAGGGATGGTCAGGAGGCTGTGGCGTGTGTGT	224 yAsnalaProProAsnSerPheTyrArgalaLeuTyrProLysIleileGlnAspileG1 244  [	284 uArgAspAsnThrileLysileTrpAspLysAsnThrLeuGluCysLysArgileLeuTh 304 1028 TGGAGACAACACCATGGGATAAAAGCACACTGGAATGCAAGGGGATTCTCAC 1087 304 rGlyHisThrGlySerValLeuCysLeuGlnTyrAspGluArgValIleIleThrGlySe 324 1088 GGGCCACGGGCTCCTGTGTCTCTGGATGAAGGAGGTATTTCAC 1147 324 rSerAspSerThrValArgValTrpAspValAsmThrGlyGluMetLeuAsmThrLeuIl 344	TCGGACTCCACCGTCAGAGTGTGAAATGCAGGTGAGATGTAAACA HishisCysGlualavalleuHisLeuargPheasnasnGlymetmetVal1 HishisCysGlualavalleuHisLeuargPheasnasnGlymetmetVal1 CaccactGTGAAGCCGTTCTGCACCTGCGCTTCAATAATGGCATGATGGTGF LYSASPARGSEXIIeAlaValTrpASpMetAlaSerProThraspIIeThrI AAAGACCGTTCCATCGCTGTGGGATATGGCTTCCCCAACTGACATCACCC	384 gValLeuValGlyHiSArgAlaAlaValASnValValAspPheAspAspLySTyrIleVa 404	424 gThrLeuAsnGlyHisLysargGlyIleAlaCysLeuGlnTyrArgAspArgLeuValVa 444  1448 GACCCTAAATGGGCACAAGCGTGGCATCGCCTGTTTGCAGTACAGAGACAGGCTGGTGGT  1508 GACCGTCCTCTGACAAGCGTGGCATGTGATTGATACAGAGACAGGCTGGTGGT  1508 GAGCGGCTCCTCTGACAACCGTCAGGCTGTGGGACATAGATGGTGGTGGTGGTGCTGGTGGTGGTGGTGGTGGTGGTGGT

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                                                                                                                        81 ATGGACCCGGCAGAGGCGGTGCAGGAGAAAGCGCTTAAGTTTATGTGCTCTATGCCC 140
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                                                                                       1 MetAspProAlaGluAlaValLeuGlnGluLysAlaLeuLysPheMet
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Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchiconi, L., Mashima, J., Mazarelli, J., Monbaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakomotoo, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-Oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wunshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs

Nature 420, 563-573 (2002)

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Please visit our web site for further details
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81. _1900
/note="beta-transducin repeat co(MGD|MGI:1338971, GB|NM_009771,
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/mol_type="mRNA"
/strain="C57BL/6J"
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erSerAspSerThrValArgValTrpAspValAsnThrGlyGluMetLeuAsnThrLeuI

CCTCAGACTCCACCGTCAGAGTGTGGGGATGTAAATGCAGGTGAGATGCTAAACACACTTGA leHisHisCysGluAlaValLeuHisLeuArgPheAsnAsnGlyMetMetValThrCysS

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324

384 rgValLeuValGlyHisArgAlaAlaValAsnValValAspPheAspAspLysTyrIleV

GGGTGCTGGTGGGACACCGAGCTGCGGTCAATGTTGTAGACTTTGATGACAAGTACATCG

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erLysAspArgSerIleAlaValTrpAspMetAlaSerProThrAspIleThrLeuArgA

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TTTCTGCCTCTGGAGATAGAACCATAAAGGTGTGGAACACAAGTACCTGTGAATTCGTAA rgThrLeuAsnGlyHisLySArgGlyIleAlaCysLeuGlnTyrArgAspArgLeuValV 1461 GGACCCTAAATGGGCACAAGCGTGGCATCGCCTGTTTGCAGTACAGAGACAGGCTGGTGG alSerGlySerSerAspAsnThrIleArgLeuTrpAspIleGluCysGlyAlaCysLeuA

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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakaa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, T., Hara, A., Fukunishi, Y., Konno, H., Kachdo, S., Yamanaka, I., Saito, T., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischman, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Kochiwa, H., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Anno, H., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Anno, H., Baldarelli, R., Barsh, G., Bisholi, M., Gustincioh, S., Hill, D., Hetcher, C., Fujita, M., Gariboldi, M., Gustincioh, S., Hill, D., Hofmann, M., Hume, D. A., Kaniya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Hofmann, M., Rodriguez, T., Sakanoco, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Stocch, K.F., Suzuki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y. Punctional annotation of a full-length mouse cDNA collection of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the stock of the 
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                                                         Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itch,M., Komo,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishi,Y., Nakamura,S., Hazama,M., Nishino,H., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegani,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watshikayi,K., Okazaki,Y., Musamatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-184-format sequencing pipeline with 384 multicapillary sequencer 2053013
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs

Nature 420, 563-573 (2002)
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1101 GGGCCACACGGGCTCCGTCCCTGTGTCTGCAGTACGATGAGAGGCTGATCATCACAGGCT 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAAAGACCGTTCCATCGCTGTGTGGGATTTGGCTTCCCCCAACTGACATCACCCTCAGGA 1340
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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TGAGCGGAGCCTATGATGAGAAATTAAAGTGTGGGATCTTATGGCTGCTTTGGACCCGC

rgAlaProAlaGlyThrLeuCysLeuArgThrLeuValGluHisSerGlyArgValPheA

rgleuGlnPheAspGluPheGlnIleValSerSerSerHisAspAspThrIleLeuIleT

alSerGlyAlaTyrAspGlyLyslleLysValTrpAspLeuValAlaAlaLeuAspProA

rgValLeuGluGlyHisGluGluLeuValArgCysIleArgPheAspAsnLysArgIleV

1581 484 1641 504 1701 524

464

544 rpAspPheLeuAsnAspProAlaAlaGlnAlaGluProProArgSerProSerArgThrT

1761

1881 ACACCTACATCTCCAGA 1897

564 yrThrTyrileSerArg

Carninci, P. and Hayashizaki, Y. High efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 92770253 10349636

musculus (house mouse)

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HTC, CAP trapper

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TACTGTTTACAGTACGACGACCAGAAGATAGTCAGCGGCCTTCGAGACAACACCATCAAG
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                                                                                                                                                                                 AlaAlaGluLeuValCysLysGluTrpTyrArgValThrSerAspGlyMetLeuTrpLys
                                                                                                                                                                                                                                    GCTGCTGAGCTGTGTGGTATGGTACCGCGTGACGTCGGACGCCATGCTGTGGAAA
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/db_xref="FANTOM DB:D330027D11"
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|MOI:1338871, GB|NM_009771, evidence: BLASTN, 100%,
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Becompic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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IACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDG
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Fax:81-45-503-9216)

Fax:B1-45-503-9216

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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose Passistance we gratefully acknowledge.

Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/.

URL:http://fantom.gsc.riken.go.jp/.

1. .3824
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 3824)
                                                                                                                                                                                                                                                                                                Bono, H., Carninci, P.,
                                                                                                                                                                                                                                                                   Adachi, J. Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fayashida, K., Hayatsu, N., Hiramcto, K., Kagawa, T., Hirozane, T., Hotoni, R., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nokamira, M., Nishi, K., Nomura, Y., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saitoh, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tarakada, T., Tomaru, A., Toya, T., Yasunishi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
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100%length, match=1587)
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A., Kamiya, M., Lee, N. H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Milming, L., Wynshaw-Boris, A., Yoshda, K. Hasegawa, Y., Kawaji, H., Kottski, S., Bromettions, L., Matshiaki, Y., Bromettions, L., Matshiaki, Y., Bromettions, L., Rawail, H., Bromettions, L., Rawail, H., Bromettions, L., Matshiaki, Y., Bromettions, L., Kottski, S., Brometti, Y., Brometti, Y., Rawail, H., Kottski, S., Brometti, Y., Rawail, H., Kottski, S., Brometti, Y., Rawail, M., Kawail, M., Rodriguez, C., Whittaker, C., Willing, L., Kottski, S., Brometti, Y., Rawail, M., Kawail, M., Brometti, R., Brometti, M., Brometti, M., Rodriguez, C., Whittaker, C., Willing, L., Kottski, S., Brometti, Y., Rawail, M., Rodriguez, C., Whittaker, C., Willing, M., Rodriguez, C., Whittaker, C., Willing, M., Rodriguez, M., Rawail, M., Kottski, S., Brometti, M., Rodriguez, C., Whittaker, C., Willing, M., Kottski, S., Brometti, M., Rodriguez, M., Kawail, M., Kottski, S., Brometti, M., Kawail, M., Kawail, M., Kawail, M., Kottski, S., Brometti, M., Kawail,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishiner, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwaji, K., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format General of pipeline with 1384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus 3 days neonate thymus CDNA, RIKEN full length enriched library, clone:A630019L11 product:F-BOX/WD-REPEAT PROTEIN 1B (F-BOX AND WD-REPEATS PROTEIN BETA-TRCP2) homolog [Homo sapiens], full
           1708 AAAATTAAAGTGTGGGATCTTATGGCTGCTTTGGACCCGCGTGCTCCAGCAGGGACTCTC 1767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The FANTOM Consortium and the RIKEN Genome Exploration Research
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Nature 409 (6821), 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                 511 CysleuArgThrLeuVal 516
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CD500760
CD46-H04.xld-t SHGC-CDA Gasterosteus aculeatus CDNA clone
CDA46-H04 5', mRNA sequence.
CDA46-H04 5', mRNA sequence.
CD500760
CD500760.
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CD500760.
Gasterosteus aculeatus (three spined stickleback)
Gasterosteus aculeatus
Gasterosteus aculeatus
CTANACHORIA (TANACHORIA)
SMARYOLA: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Percomorpha; Gasterosteidostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteidosteis
Gasterosteidae; Gasterosteus.
ST (Dases I to 1136)
Kingsley, D.M., Peichel, C., Balabahdra, S., Grimwood, J., Dickson, M., Schmutz, J. and Myers, R.M.
Schmutz, J. and Myers, R.M.
Farressed sequence tags from Gasterosteus aculeatus
                              AAAGTGCTAACGGGCCACACAGGCTCTGTCCTCTGCCTCCAGTATGATGAGGGGAGTCATT
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363 GCGGTTCTTCACCTACGCTTCGCCAACGGATTGATGGTCACCTGCTCCAAGGACCGCTCG 422
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amblibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
1 (Dases 1 to 924)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                               369 IlealaValTrpAspMetAlaSerProThrAspIleThrLeuArgArgValLeuValGly
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                                                                                                          483 CACCGGGCTGCTGTCATTGTGTGGTCGACTTTGATGACAAATACATTGTGTCCGCCTCAGGG
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/tissue_type="heads and internal organs combined"
/dev stage="adult"
/dev stage="adult"
/clone_lib="SHGC-CDA"
/note="Vector: lambda ZAP Express/pBK-CMV; Site_1: EcoRl
/soften DNA library was generated using the ZAP-cDNA method organ cDNA library was generated using the ZAP-cDNA method by Stratagene. First strand cDNA synthesis was primed with a a 50 bp linker primer containing an oligo dT sequence preceded by a synthetic XhoI site. 5 prime adaptors were used containing an EcoRl cohesive end. The finished cDNAs were inserted in to the ZAP express vector unidirectionally in the sense orientation with respect to the lack promocer of pBK-CMV. An amphified library was prepared from approximately 3 million primary clones in the lambda ZAP Express vector. In vivo excision was then used to generate individual pBK-CMV phagemid clones for
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                          HHMI and Department of Developmental Biology Stanford University School of Medicine Beckman Center B300, 279 Campus Drive, Stanford, CA Tel: 650 725 5954 Fax: 650 725 7739 Fax: 650 725 7739 Fax: 650 725 7739 Fax: 640 Fax: 650 725 7739 Fax: 650 725 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 Fax: 670 7739 F
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Conservative:
Mismatches:
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AL898993 AGC-egg Silurana tropicalis CDNA clone TEgg019e21 3', mRNA
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/clone="TE9019621"
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/lab_host="Escherichia coli XLI-blue"
/clone lib="xGG-egg"
/note="Vector: pC8107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNĀ from egg.
EcoRI-NotI cut cDNA was then ligated into pC8107 with
EcoRI at the 5' end and NotI at the 3' end"
232 c 199 g 232 t
                   750
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Silurana tropicalis
Silurana tropicalis
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Amphibia, Batrachia, Anura; Mesobatrachia, Pipoidea, Pipidae; Kenopodinae, Silurana
1 (bases 1 to 895)
1 (bases 1 to 895)
Sanger Xenopus tropicalis EST project 2002
Unpublished
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                                                                                                                               -ProAla-GlyThrLeuCysLeuArg-ThrLeu-ValGluHisSerGlyArgValPhe--
                 CTGGAAGGACATGAAGTGGTCCGGTGCATCCGCTTTGATAACAAGAGAATAGTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.
Location/Qualifiers
1. .895
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anger Xenopus tropicalis EST project 2001
TROPICALIS SEQUENCE ID: TEGG019e21.qlkT7
Sequencing primer: T7
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Matches:
Conservative;
Mismatches:
Indels:
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                   691
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DB:
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KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                        | 1. .924
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| /db_xref="taxon:8355"
| /don=="MAGE:6860098"
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| /clone lib="NICHD XGC 001"
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| size 2.2 kb. Constructed by Life Technologies."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspSerThrValArgValTrpAspValAsnThrGlyGluMetLeuAsnThrLeuIleHis 345
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2278
5
6
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
60
 Plate: LLAM14473 row: o column
High quality sequence start: 16
High quality sequence stop: 717.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-168B-2 (1-569) x CA985560 (1-924)
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1407.50
96.22%
95.53%
46.39%
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us-09-601-168b-2.rst

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228 ProAsnSerPheTyrArgAlaLeuTyrProLysIleIleGlnAspileGluThrIleGlu 247
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: XG clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1498 row, G.D. column: 05
High quality sequence start: 15
High quality sequence start: 15
Location/Qualifiers
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19
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Matches:
Conservative:
Mismatches;
Indels:
                                                                                                                                                                                                                /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
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MAGES:68658574 S', mRNA sequence.
                                        LeubsnThrLeuIleHisHisCysGluAlaValLeuHisLeuArgPheAsnAsnGlyMet 359
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Email: cgapbs-romail.nih.gov
Tissue Procurement: N. Garrett, P. LeMaire, A.M. Zorn, and J.B.
Gurdon (Wellcome/CRC Institute)
CDNA Library Preparation: N. Garrett, P. LeMaire, A.M. Zorn, and
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    834 ATCATAACCGGCTCTTCTGACTCTACCGTCCGGGTTTGGGACGTAAACACAGGAGAAATG
                                                                           774 TIGAACACICIGATICACCACIGIGAGGCIGIGCIACATITGAGGITTAACAAIGGIAIG
                                                                                                                  MetValThrCysSerLysAspArgSerIleAlaValTrpAspMetAlaSerProThrAsp
                                                                                                                                                                                                                                654 ATCACATTACGAAGAGTTCTAGTAGGCCACCGAGCTGCCGTAAATGTGGTGGACTTTGAT
                                                                                                                                                                                                                                                                                                            GACAAGTACATAGTCTCTGCTCTGGTGATCGAACAATAAAGGTTTGGAACACCAGTACA
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
Tumor Gene Index
Unpublished
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Xenopus laevis
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US-09-601-168B-2 (1-569) x CB244526
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Best Local Similarity:
Query Match:
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/mol_type="mRNA"
/strain="C57Bi./6"
/db_xref="texon:10090"
/db_xref="texon:10090"
/clone="IMAGE: 6833135"
/tissue_type="wmbro la"5:14.5,16.5,17.5dpc"
/dev_stage="mbryo la"5.14.5,16.5,17.5dpc"
/dev_stage="mbryo la"5.14.5,17.5dpc"
/dev_stage="mbryo la"5.14.
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UI.M-FYO-cdq-k-22-0-UI.rl NIH_BMAP_FYO Mus musculus cDNA clone
UI.MACE: 6833135 5', mRNA sequence.
CB244526
CB244526.1 GI:28366170
EST.
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Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the IIM.A.G.E. Consortium/LINL at:
447
                                                                                                                                                                                                                                                                            GlyHisGluGluLeuValArgCysIleArgPheAspAsnLysArgIleValSerGlyAla 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Nat.-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                      GlyHisLysArgGlyIleAlacysLeuGlnTyrArgAspArgLeuValValSerGlySer
                                                                                                        670 TCTGACAC-ACAATCAGATTGTGGGATATTGAATGCGGTGCATGTTTGCGGGGTCTGGAA
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                                                                                                                                                                              SerAspAsnThrileArgLeuTrpAspIleGluCysGlyAlaCysLeuArgValLeuGlu
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Contact: Robert Strausberg, Ph.D.
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directionally into pXX-Asc vector. The library tag directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mentcal Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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Matches:
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BQ444188 1778 bp mRNA linear EST 29-MAY-2002 UI-M-EXO-bxj-1-06-0-UI.rl NIH BMAP_EXO Mus musculus cDNA clone IMAGE:5709077 5', mRNA sequence.
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Email: gapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDN Library preparation: Dr. M. Bento Soares, University of Iowa
CDN Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC Clone distribution information can be
AGCTTGGAATGTTTGAAAGTGCTAACGGGCCACACAGGCTCTGTCCTCTGCCTCCAGTAT 120
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Mus musculus
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                 316 AspGluArgValIleIleThrGlySerSerAspSerThrValArgValTrpAspValAsn
                                                                               356 AsnAsnGlyMetMetValThrCysSexLysAspArgSex1leAlaValTrpAspMetAla
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/site_2: Not l: The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNa was size fractionated on a 1% agarcee gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cond primer accordaning a Not I site. Double stranded cond primer accordaning a Not I site. Double stranded cond with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCCACGAC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
                                                 p mRNA linear EST 14-MAR-2002
BMAP_EHOp Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                               Bmail: cgapbs-r@mail.nih.gov
Trisue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CLORE Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (Bases 1 to 810)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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                                              BM944304
UI-M-EHOp-bvg-m-18-0-UI.rl NIH_B
IMAGE:5695673 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db xref="taxon:10090"
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Location/Qualifiers
1. .810
                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                              BM944304.1 GI:19427889
EST.
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EST 27-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTCACGGGCCACACGGGCTCCGTCTGTGTTGCGTACGATGAGAGGGTGATCATC 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopodinae; Xenopus.
1 (bases 1 to 1002)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nin.gov
Tissue Procurement: N. Garrett, P. LeMaire, A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute)
cDNA Library Preparation: N. Garrett, P. Lemaire, A.M. Zorn, a. J.B. Gurdon (Wellcome/CRC Institute)
cDNA Library Arrayed by: The II.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: XGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 LeuThrGlyHisThrGlySerValLeuCysLeuGlnTyrAspGluArgValIlelle 321
                                                                                                                                                                                                                                     GGCCTTCGAGACAC-ACCATCAAGATCTGGGANTAAAGCACACTGGAATGCAAGCGGATT
                                                                                                               243 IleGluThrIleGluSerAsnTrpArgCysGlyArgHisSerLeuGlnArgIleHisCys
                                                                                                                                                                                                                                                                                                                 ArgSerGluThrSerLysGlyValTyrCysLeuGlnTyrAspAspGlnLysIleValSer
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                                                                                                                                                                                                                                                                                                                                                                                                                             GlyLeuArgAspAsnThrIleLysIleTrpAspLysAsnThrLeuGluCysLysArgIle
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found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13766 row: d column: 24
High quality sequence start: 98
High quality sequence stop: 710.
Location/Qualifiers
1. 1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
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EST.
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                                                                                                                                             481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
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/clone="Infate: 50 pc"
/dev. stage="whole brain"
/dev. stage="whole brain"
/dev. stage="whole brain"
/dev. stage="whole for in the property is a pc."
/dev. stage="mbryo is. 5 pc."
/lab hose="Dilbe" III phage resistant)"
/clone lib="NIH BMAP_EXO"
/clone lib="NIH"
/clo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TyrLeuAspAlaLysSerLeuCysAlaAlaGluLeuValCysLysGluTrpTyrArgVal 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrSerAspGlyMetLeuTrpLysLysLeuIleGluArgMetValArgThrAspSerLeu 202
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                              http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
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found through the I.M.A.G.E. Consortium/LLNL at:
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Matches:
Conservative:
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Indels:
                                                                                                                                                                                                    /organism="Mus musculus"
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                                                                                                                  Location/Qualifiers
]. .778
                                                                                                                                                                                                                               /mol_type="mRNA"
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IMAGE:6802203 5',
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                              252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AspLysAsnThrLeuGluCysLysArglleLeuThrGlyHisThrGlySerValLeuCys 312
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                                                                                                                                                                                                                                                                CTAGATCACATAGCAGAAAACATCCTTTCATACCTGGACGCAAGGTCATTGTGTTTTCGCA
                                                                                                                                                                                                                                                                                                                                                                                                              GGTCAATATCTATTTAAAAACAAACCTCCAGATGGGAAAACGCCACCAAATTCCTTCTAC
                                                                                                         SerTyrGluLysGluLysGluLysGluLysGluLysTyrPheGluGlnTrpSerGluSerAsp
                                                                                                                      IleGluArgMetValArgThrAspSerLeuTrpArgGlyLeuAlaGluArgArgGlyTrp
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                  (1-1002)
                                                                                   (1-569) x CA971789
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2.57e-135
1323.50
92.41%
88.97%
43.62%
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ocal Similarity:
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CA975032 935 bp mRNA linear EST 06-JAN-2003 AGENCOURT\_11076265 NCI\_CGAP\_ZEMb2 Danio rerio cDNA clone

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/note=1: pCMV-SPORT6.cdb; Site 1: BCORV6.cdb; Site_2: DCORV6.cdb;                                                                                                                                                             Danio rerio (zebrafish)
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Danio rerio
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Danio rerio
Danio relio
Danio relio
Actinopterygii, Neopterygii, Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 935)
11 (hases 1 to 935)
NHI-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Contract: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Leonard I. Zon, M.D.
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayad by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMA4323 row: c column: 02
High quality sequence start: 24
High quality sequence stop: 652.
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Best Local Similarity:
Query Match:
DB:
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Longublished
Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lih. University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
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850 bp mRNA linear EST 27-NOV-2002 UI-M-FYO-ccy-f-17-0-UI.rl NIH BMAP_FYO Mus musculus cDNA clone IMAGE: 6826098 5', mRNA sequence.
CA327271

CA327271.1 GI:24545369
EST.
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                                                                                                                      ArgSerIleAlaValTrpAspMetAlaSerProThrAspIleThrLeuArgArgValLeu
                                                                                                                                                                                                                                                                    ValGlyHisArgAlaAlaValAsnValAspPheAspAspLysTyrIleValSerAla
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//dev stage="1, 5, and 15 days newborn"
//dev stage="1, 5, and 15 days newborn"
//dev stage="1, 5, and 15 days newborn"
//deb host="Hill (TI phage resistant)"
//dev stage="1, 5, and 15 days newborn"
//dep in="1" (Tipe library was constructed according
Stre 2: Not 1, The library was constructed according
Bonaldo. Lennon and size fractionated on a 1% agarose
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Notl and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    744 bp mRNA linear EST 28-MAR-2003
UI-M-GHO-cel-p-18-0-UI.rl NIH EMAP GHO Mus musculus cDNA clone
IMAGE: 6841315 5', mRNA sequence.
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Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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National Institutes of Health, Mammalian Gene Collection
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## SUMMARIES

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                                                                                                                                                                                                                    e present invention describes an F-box motif protein of ubiquitin gase SCF complex which promotes the ubiquitination of IkappaB or ta-catenin and is constituted by Skpl protein, Cull protein and a mplex (SCF complex) of F-box protein containing F-box motif and Wato peat motif and has the amino acid sequence of 45 residues (ABB1881) one of two ScP residue sequences (AAB12812, which is mouse ubiquitin gase FWD1 protein) and (AAB12813, which is human beta-transducin peat containing protein (beta-TrCP). The F-box protein can be used for e gene therapy of colon cancer by baing recombined to a virus vector. esent invention.
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                                                     crercaraceregareceaaareacrarereceeerecreaacrirererecaaggaareerae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence encodes a human beta-transducin repeat containing tein (beta-TrcP). The protein directs proteins to the proteosome radation pathways. The protein is able to interact with the Vpu tein of human immune deficiency virus-1 (HIV-1), cellular proteins ppaB or beta-catenin (bC) and/or protein Skplp. The protein controls quitinylation of phosphorylated protein and thus their targeting to teosomes for degradation. Depending on Whether the process is thibited or promoted, the result may be delayed breakdown of Cp4 (in es of HIV-1 infection); increased activity of IkB (and thus reduced ivity of NFkappaB) and increased degradation of mutant bC in tumour
                                      IleleulleTrpAspPheLeuAsnAspProAlaAlaGlnAlaGluProProArgSerPro
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521 ArgValPheArgLeuGlnPheAspGluPheGlnIleValSerSerHisAspAspThr
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/note= "beta-transducin repeat containing protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NA encoding a human beta-transducin repeat containing protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / human beta-transducin repeat containing protein and its gments useful as, or to screen for, antiviral, antitumour, i-inflammatory and anti-Alzheimer's agents
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all M, Margottin F;
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              patients. The beta-TrcP protein, and its active peptide fragments, or inuclaic acid, are used to screen for anti HIV-1 agents (antivirals), antitumour agents that disrupt cell cycle regulation or protein degradation in human tumour cells, and anti-inflammatcry agents that disrupt activation by NFkappaB. Fragments of the protein are also useful for treating osteo-articular inflammation or acute inflammation associated with release of tumour necrosis factor.

(Updated on 20-MAR-2003 to correct PA field.)
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Human beta-TrCP coding sequence

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HisCysArgSerGluThrSerLysGlyValTyrCysLeuGlnTyrAspAspGlnLyslle
                          CACTGCCGAAGTGAAACAAGCAAAGGAGTTTACTGTTTACAGTATGATGATCATCAGAAAATA
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DNA; 2151

151229 standard;

(first entry)

SEP-2000

5,1229;

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This DNA encodes human beta-TrCP, an F-box/ND protein family member, which has been shown to have homology to human E3 ubiquitin ligase (E3). E3 enhances ubiquitination of phosphorylated I-kappa-B, an inhibitor protein of nuclear factor kappa-B (NF-kappa-B). Understanding I-kappa-B degradation via the ubiquitin pathway is useful for identifying modulators of this process for use in treating diseases associated with activation of NF-kappa-B. In vitro analysis suggests that deletion of the F-box results in a protein that functions as a dominant negative molecule in vivo. Transfert over-expression of edication mutant) inhibited the degradation of endogenous I-kappa-B path in stimulated Jurkat cells, resulting in accumulation of phosphorylated in stimulated Jurkat cells, or screen for modulators of NF-kappa-B cotivity. E3 and beta-TrCP can be used to modulate NF-kappa-B to treat inflammatory diseases, autoimmune diseases, cancer and viral infections.
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                             E3 ubiquitin ligase; beta-TrCP; F-box; WD protein; I-kappa-B; inhibitor; nuclear factor kappa-B; NF-kappa-B; degradation; modulator; anti-viral; anti-inflammatory; immunosuppressive; cytostatic; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptide enhancing phosphorylated lkappaB ubiquitination useful streating disorder associated with NF-kappaB activation e.g. cancer, comprising amino acid sequence of human E3 ubiquitin ligase or its
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                                                                                                                                                                                                                                                                                                                                                                                         Davis
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                                                                                                                                Location/Qualifiers
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                      190 AGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGTATGTTTAGCA
                                                       SerThrAlaMetLysThrGluAsnCysValAlaLysThrIysLeuAlaAsnGlyThrSer
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ovel nucleic acid for screening compounds useful for treating roliferative and differentiative disorders such as cancer and immune isorders comprises sequences encoding ubiquitin ligases
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ısclosure; Figure 3b, 3c, 3d; 245pp; English.

ingleic acids encoding substrate-targeting subunits of ubiquitin igases with F-box motifs (F-box proteins) are useful for diagnosiss proliferative and differentiated related disorders by measuring 3P gene expression. Cells expressing such proteins or leir fragments are useful for screening compounds. The compounds re agonists or antagonists, which are useful for treating a rolliferative or differentiative disorder in a mammal such as reast, ovarian and prostate cancer and small cell lung carcinoma ridiovascular diseases and inflammantory disorders. PBP protein, analogs, derivatives and their subsequences, anti-FBP antibodies also useful in diagnosis of the disorders.

quence 2151 BP; 628 A; 467 C; 513 G; 543 T; 0 other;

151 69	SPheMetAsnSerSerGlu 20 	SProGluLysAsnSerLeu 40	Cysteunia o IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ACTTGCCAATGGCACTTCC 309 GGULVSGUUDYSGUULEU 100 	GluPheValGluHisLeu 120   GluPheValGluHi	rTyrLeuLysProMetLeu 140 	OHISILGAlaGluAsnIle 160	UValCysLysGluTrpTyr	JArgMetValargThrasp 200 	nTyrLeuPheLysAsnLys 220
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5.66e-303 3034.00 100.008 .ty: 100.00\$ 21 21 -569) x AAZ93350	pproAlaGluAlaVall	uAspCysAsnAsnGly(                \AGACTGTAATAATGGCC	nintiyinshsercys, GACATACAACAGCTGTC IRAlaMetLysThrGlw	rtecrateaacacreaca tilevalProLysglm 	llrysTyrPheglugln: 	erGlnMetCysHisTyrd 	cgAspPhelleThrAlai 	erTyrLeuAspAlaLys 	alThrSerAspGlyMet. 	euTrpArgGlyLeuAla
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2	81 ValSerGlyLeuArgAspAsnThrIleLysIleTrpAspLysAsnThrLeuGluCysLys 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e F-box proteins are a family of ubiquitin ligases (SCF ubiquitin jases) which can be used for the targetted degradation of a target bypeptide in vivo. Targetted degradation is achieved by expressing a ubiquitin ligase in a cell linked to the interaction domain of a target polypeptide and thereby recruiting the target polypeptide and strengt polypeptide of a target polypeptide and for decreasing or breasing the level of a target polypeptide and for creating and ressing a destabilized polypeptide which is subjected to SCF listed proteolysis. Degrading any desired protein in a cell is sful for preventing or treating diseases caused by the presence of normal amount of the specific polypeptides, for drug discovery and regene therapy. Diseases treated include cancer, by degradation of copporations. The method provides a quick and easy proteins. The method provides a quick and easy can degraded at all stages, or a specific stage, of development in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rgeting degradation of polypeptide useful for treating cancer and her proliferative disorders, involves conjugating polypeptide with iquitin protein ligase or inhibiting ubiquitination using organic apound
                                                                                                                                                                                                iquitin ligase; SCF; F-box protein; targeted degradation; stabilisation; proteolysis; drug discovery; gene therapy; cancer; coprotein; Huntington's disease; gene knockout; delivery systems;
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The invention relates to methods of altering the polypeptide levels in a cell, using proteins selected from S-phase kinase associated proteins 1 and 2 (SKP1, SKP2), SKP2-like proteins (EP) and CUL-1 (a member of the cullin/ CDC51 family of proteins). The method is useful for altering the polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for detecting tumours, and in monitoring tumor treatment in a mammal. Agents that modulate interactions between SKP and target proteins are useful for
                                                                                  Modulating polypeptide levels in a cell, diagnosing and treating tumor, involves altering levels of proteins such as S-phase kinase associated proteins 1, 2 and cullin/CDC53 proteins -
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                                            ValThrCysSerLysAspArgSerIleAlaValTrpAspMetAlaSerProThrAspIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phase kinase associated protein; SKP1; SKP2;
6-1; cullin; CDC53; p27; cyclin E; Max; Mad;
1; Bc1-2; tumour; cytostatic; ds.
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The invention relates to screening compounds useful for the treatment of proliferative or differentiative disorders comprising detecting a change in the activity of SRp2 (F-box protein). The method is useful for screening compounds for the treatment of proliferative or differentiative disorders, particularly cancer. These compounds include small molecules, or compounds or derivatives or analogues of the new ubiquitin ligases. The compounds are useful for treating diseases such as cancer (e.g. breast cancer, prostate cancer or ovarian cancer, lymphoma, small cell lung carcinoma or parathyroid adenomas), major opportunistic infections, immune disorders, certain cardiovascular diseases or inflammatory disorders. This polymolectide sequence represents the oDNA encoding an F-box protein (FBP) of the invention.
                                                                                                                                                                                                                              Cytostatic, immunomodulator, cardiant, antiinflammatory; antimicrobial, proliferative, differentiative disorder, Skp2, F-box protein, cancer, ubiquitin ligase, breast cancer, prostate cancer, ovarian cancer, small cell lung carcinoma, immune disorder, parathyroid adenoma, FBP; inflammatory disorder, lymphoma, major opportunistic infection, certain cardiovascular disease; human, gene, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening compounds for treating proliferative disorders, e.g. breast cancer or prostrate cancer, infections or immune disorders, comprises detecting a change in the activity of Skp2 with either p27 or Cks1
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1570 TIGGACCCCCGTGCTCCTGCAGGGACACTCTGTCTACGGACCCTTGTGGAGCATTCCGGA 1629
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                 LysTyrIleValSerAlaSerGlyAspArgThrIleLysValTrpAsnThrSerThrCys
                                                                                                                                                                    .690 ATCCTCATCTGGGACTTCCTAAATGATCCAGCTGCCCAAGCTGAACCCCCCCTTCCCCT
                                                                                  GluPheValargThrLeuAsnGlyHisLysArgGlyIleAlaCysLeuGlnTyrArgAsp
                                                                                                                  1330 GAATITGTAAGGACCTTAAATGGACACAAACGAGGCATTGCCTGTTTGCAGTACAGGGAC
                                                                                                                                                                                                                                               GCATGTTTACGAGTGTTAGAAGGCCATGAGGAATTGGTGCGTTGTATTCGATTTGATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IleLeuIleTrpAspPheLeuAsnAspProAlaAlaGlnAlaGluProProArgSerPro
                                              1270 AAGTACATTGTTTCTGCATCTGGGGATAGAACTATAAAGGTATGGAACACAAGTACTTGT
                                                                                                                                                    ArgleuValValSerGlySerSerAspAsnThrIleArgLeuTrpAspIleGluCysGly
                                                                                                                                                                                                                    461 AlaCysLeuArgValLeuGluGlyHisGluGluLeuValArgCysIleArgPheAspAsn
                                                                                                                                                                                                                                                                                     LysArgIleValSerGlyAlaTyrAspGlyLysIleLysValTrpAspLeuValAlaAla
                                                                                                                                                                                                                                                                                                                                                       LeuAspProArgAlaProAlaGlyThrLeuCysLeuArgThrLeuValGluHisSerGly
                                                                                                                                                                                                                                                                                                                                                                                                                         ArgValPheArgLeuGlnPheAspGluPheGlnIleValSerSerSerHisAspAspThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel complex of protein-protein interactions in adipocyte cells for identifying compounds that modulate the protein-protein interactions and useful for treating obesity and metabolic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cDNA encoding bait protein beta-TrCP1.
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                                                                                                                         AGCACTGCTATGAAGACTGAGAATTGTGTGGCCAAAACAAAACTTGCCAATGGCACTTCC
                                                                                                                                                                                                                                                                                                                                                                     GlnArgAspPheIleThrAlaLeuProAlaArgGlyLeuAspHisIleAlaGluAsnIle
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                                ArgGlnThrTyrAsnSerCysAlaArgLeuCysLeuAsnGlnGluThrValCysLeuAla
                                                                AGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAAGAAACAGTATGTTTAGCA
                                                                                                  SerThrAlaMetLysThrGluAsnCysValAlaLysThrLysLeuAlaAsnGlyThrSer
                                                                                                                                                                    SerMet11eValProLysGlnArgLysLeuSerAlaSerTyrGluLysGluLysGluLeu
                                                                                                                                                                                      AGTATGATTGTGCCCAAGCAACGGAACTCTCAGCAAGCTATGAAAAGGAAAAGGAACTG
                                                                                                                                                                                                                                   CysValLysTyrPheGluGlnTrpSerGluSerAspGlnValGluPheValGluHiSLeu
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laim 2; Page -; 125pp; English.

he invention relates to a complex of protein-protein interactions forming a protein-protein interaction map, PIM) in adipocyte cells as sincined in the specification, or polynucleotides in adipocyte senceding the teracting polypeptides. Also included are a recombinant cell expressing the teracting polypeptides and a method of selecting a modulating compound adium containing a modulating a recombinant host cell on a selective spression of which is toxic for the recombinant host cell which is ansigned weeters, where the first vector comprises a summin and the second vectors, where the first vector comprises a summin and the second vector comprising a polynucleotide encoding a scond hybrid polypeptides the second vector comprising a polynucleotide encoding a scond hybrid polypeptides the recombinant host cell (i.e. using the yeast two-hybrid polypeptides and selecting the modulating compound which inhibits the rowth of the recombinant host cell (i.e. using the yeast two-hybrid to protein or metabolic disconders and useful for treating obesity and tabolic disconders eng. non-insulin dependent dispetes mellitus, rewning obesity or metabolic diseases. The interactions between the proteins of the complex further define a member of the protein summins, SiD. The present sequence encodes a member of the protein when the present sequence encodes a member of the protein very brid assay.

## quence 2151 BP; 628 A; 467 C; 513 G; 543 T; 0 other;

nt Scores:

0	5.66e-303	Length:	2151
	3034.00	Matches:	269
Similarity:	100.00%	Conservative:	0
cal Similarity:	: 100.00%	Mismatches:	0
atch:	100.00%	Indels:	0
	24	Gaps:	0
01-168B-2 (1-5	01-168B-2 (1-569) x ABS51009 (1-2151)	(1-2151)	
1 MetAspP	roAlaGluAlaValL	1 MetAspProhlaGluAlaValLeuGlnGluLysAlaLeuLysPheMetAsn	LysPheMetAsn
70 ATGGACC	CGGCCGAGGCGGTGC		CAAGTTTATGAAT
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		TO DESCRIPTION OF THE PROPERTY	
130 AGAGAAG	actgraataarggcg	AGAGAAGACTGTAATAGTGGCGAACCCCCTAGGAAGATAATACCAGAGAAG	AATACCAGAGAAG
41 AraGlnT	hrTvrAsnSerCvsA	JaAroLeuCysLeuAsı	nGl nGluThrVal

Н	MetAspProAlaGluAlaValLeuGlnGluLysAlaLeuLysPheMetAsnSerSerGlu 2	0
70	ATGGACCCGGCCGAGGCGGTGCTGCAAGAAAGGCACTCAAGTTTATGAATTCCTCAGAG	59
21	ArgGluAspCysAsnAsnGlyGluProProArgLysIlelleProGluLysAsnSerLeu	0
130	AGAGAAGACTGTAATAATGGCGAACCCCTAGGAAGATAATACCAGAGAAGATTCACTT	189
41	ArgGlnThrTyrAsnSerCysAlaArgLeuCysLeuAsnGlnGluThrValCysLeuAla 6	0
190	AGACAGACATACAACAGCTGTGCCAGACTCTGCTTAAACCAGAAAGAGTGTTTAGCA	249
61	SerThrAlaMetLysThrGluAsnCysValAlaLysThrLysLeuAlaAsnGlyThrSer 8	0
250	AGCACTGCTATGAAGAATTGTGTGTGGCCAAAGAAAACTTGCCAATGGCACTTCC	309
81	SerMetIleValProLysGlnArgLysLeuSerAlaSerTyrGluLysGluLysGluLeu	100
310	AGTATGATTGTGCCCAAGCAACGGAAACTCTCAGCAAGCTATGAAAAGGAAAAGGAACTG	369
101	CysValbysTyrPheGluGlnTrpSerGluSerAspGlnValGluPheValGluHisLeu	120
370	TGTGTCAAATACTTTGAGCAGTGGTCAGAGTCAGATCAAGTGGAATTTGTGGAAACATCTT	429
121	11eSerGlnMetCysHisTyrGlnHisGlyHis1leAsnSerTyrLeuLysProMetLeu	140
430	ATATCCCAAATGTGTCATTACCAACATGGGCACATAAACTCGTATCTTAAACCTATGTTG	489
141	GlnArgAspPheIleThrAlaLeuProAlaArgGlyLeuAspHisIleAlaGluAsnIle	160
490	CAGAGAGATITCATAACTGCTCTGCCAGCTCGGGGATTGGATCATATCGCTGAGAACATT	549

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ογ	181	ArgValThrSerAspGlyMetLeuTrpLysLysLeuIleGluArgMetValArgThrAsp 200
Db	610	CGAGTGACCTCTGATGCCATGCTGTGGAAGCTTATCGAGAGAATGGTCAGGACAGAT 669
č da	201	201 SerbeuTrpArgGlyLeuAlaGluArgArgGlyTrpGlyGlnTyrLeuPheLysAsnLys 220 
. 6	221	ProproAsnGlvAsnAlaProProAsnSerPheTvrArdAlaLeuTvrProivsIleIle 240
. ac	730	CCTCCTGACGGGAATGCTCCTCCCAACTCTTTTTATAGAGCACTTTATCTAAATTATAA 789
ολ	241	GlnAspileGluThrileGluSerAsnTrpArgCysGlyArgHisSerLeuGlnArgile 260
Db	790	CAAGACATTGAGACAATAGAATCTAATTGGAGATGTGGGAAGACATAGTTTACAGAGAATT 849
ò	261	HisCysArgSerGluThrSerLysGlyValTyrCysLeuGlnTyrAspAspGlnLysIle 280
QD QD	850	Cactgccgaagtgaaacaagcaaaggagtttactgtttacagtatgatgatcagaaata 909
75	281	ValSerGlyLeuArgAspAsnThr11eLys11eTrpAspLysAsnThrLeuGluCysLys 300
2 (	0 1	GIANGCCGGCCTICGAGACACACATCAGGAICAGGAIAAAAACACAIIGGAAGG 909
ÇŞ t	301	ArgiteLeuinrGiyHisThrGiyeerValleuCysLeuGinTyThspGluArgVallle 320
Q C	2	CGAATICICACAGGCCATACAGGTICAGICCICIGICICCAGIAIGAIGAGAGGIGAIC 1029
δλ	321	IleThrGlySerSerAspSerThrValArgValTrpAspValAshThrGlyGluMetLeu
QQ Q	1030	ATAACAGGATCATCGGATTCCACGGTCAGAGTGTGGGATGTAAATACAGGTGAAATGCTA 1089
à	341	
Db	1090	AACACGITGATICACCATTGIGAAGCAGITCIGCACTTGCGITTCAATAATGGCATGATG 1149
δλ	361	ValThrCysSerLysAspArgSerlleAlaValTrpAspMetAlaSerProThrAspIle 380
qq	1150	GIGACCIGCTCCAAAAAICGTICCATIGCTGIAIGGGAIAIGGCCTCCCCAACIGACAII 1209
È	381	
qq	1210	ACCCTCCGGAGGGTGCTGGTCGGACACCGAGCTGCTGTCGATGTTGTTGTTGTTGTTGTTGTTGTCTCTC69
٥y	401	
Dp	1270	AAGTACATTGTTTCTGCATCTGGGATAGAACTATAAAGGTATGGAACACAGTACTTGT 1329
ζ	421	
Dp	1330	GAATTIGTAAGGACCTTAAATGGACACAAAACGAGGCAFTGCCTGTTTGCAGTACAGGGAC 1389
οy	441	
qq	1390	AGGCTGGTAGTGACTCTCTCTGACACTATCAGATTATGGGACATAGAATGTGGT 1449
δλ	461	AlaCysLeuArgValLeuGluGlyHisGluGluLeuValArgCysIleArgPheAspAsn 480
QQ	1450	GCATGTTTACGAGTGTTAGAAGGCCATGAAGGAATTGGTGGTGTTGTATTCGATTGATAGC 1509
٥٨	481	
QC	1510	AAGAGGATAGTCAGTGGGGCCTATGATGGAAAATTAAAGTGTGGGATCTTGTGGCTGCT 1569
٥'n	501	LeuAspProArgAlaProAlaGlyThrLeuCysLeuArgThrLeuValGluHisSerGly 520
qq	1570	TIGGACCCCCGTGCTCCTGCAGGGACACTCTGTCTACGGACCCTTGTGGAGGATTCCGGA 1629
č	521	ArgValPheArgLeuGlnPheAspGluPheGlnIleValSerSerSerHisAspAspThr 540

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1030 ATAACAGGATCATGGGATTCCACGGTCAGAGTGTGGGGATGTAAATACAGGTGAAATGCTA 1089
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                                                                                                                                   SerMetlleValProLysGlnArgLysLeuSerAlaSerTyrGluLysGluLysGluLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence is a cDNA obtained from Incyte clone 3239149 of JAUCTO1 library. It encodes cell signalling protein-12 (CSIGP-12). It expressed in musculo-skeletal, gastrointesinal and nervous such an expressed in musculo-skeletal, gastrointesinal and nervous such areas of CSIGP encoding nucleic acid can be used as bridisation probe for detecting CSIGP related sequences or allelic iants. Recombinant CSIGP can be produced in host cells by transforming m with genetically engineered vectors. Agonists or antagonists can be id in the treatment of cell proliferative and inflammatory disorders isociated with decreased or increased CSIGP expression. CSIGP is used in idagnosis, prevention and treatment of cell proliferative disorders ce arteriosclerosis, cirrhosis, cancer, hepatitis and inflammatory
| IleLeulleTrpAspPheLeuAspAspFroAlaAlaGlnAlaGluProProArgSerPro
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/product= "Cell Signalling Protein-12"
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PSDB; AAY44249.
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Tang YI, Liu C, Asundi V, Chen R, Mhman T, Xu C, Xue AJ, Yang Y, Zhang

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expressed in the bone marrow. The polymuclectide and the polypetide encoded by it are useful in the treatment of various immune deficiencies and disorders. The deficiencies and disorders may be genetic, may be caused by a viral (e.g. HIV), bacterial or fungal infection, or may result from an autoimmune disorder, a coagulation disorder (e.g. haemophilia), inhibition of tumour cell proliferation, suppression of an inflammatory response or treatment of a nervous system disorder such as Alzheimer's disease. Detection of the presence or increased expression of the polymucleotide or the protein it encodes is useful for the diagnosis and/or prognosis of one or more types of cancer. The polymucleotide and polypeptide can be used as nutritional sources or supplements and in the screening of chemical compounds as potential drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel bone-marrow-expressed polynucleotides and polypeptides, useful for treating e.g. cancer and immune deficiency disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence is one of 251 novel human polynucleotides
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2000US-055317
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                                                                             AACACGTTGATTCACCATTGTGAAGCAGTTCTGCACTTGCGTTTCAATAATGGCATGATG
                                                                                                                                                                  ValThrCysSerLysAspArgSerIleAlaValTrpAspMetAlaSerProThrAspIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaCysLeuArgValLeuGluGlyHisGluGluLeuValArgCysIleArgPheAspAsn
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                                      AsnThrLeuIleHisHisCysGluAlaValLeuHisLeuArgPheAsnAsnGlyMetMet
                                                                                                                                                                                                                                     1150 GIGACCTGCTCCAAAGATCGTTCCATTGCTGTATGGGATATGGCCTCCCCAACTGACATT
                                                                                                                                                                                                                                                                                                    ThrLeuArgArgValLeuValGlyHisArgAlaAlaValAsnValValAspPheAspAsp
                                                                                                                                                                                                                                                                                                                                                                       <u> ACCCTCCGGAGGGTGCTCGGACACCGAGCTGCTGTCAATGTTGTAGACTTTGATGAC</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        569
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Sequence 3220 BP; 878 A; 725 C; 770 G; 847 T; 0 other
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Matches:
Conservative:
Mismatches:
Indels:
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                   IleSerGlnMetCysHisTyrGlnHisGlyHisIleAsnSerTyrLeuLysProMetLeu 140
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                                          ATATCCCAAATGTGTCATTACCAACATGGCACATAAACTCGTATCTTAAACCTATGTTG
                                                                                         GlnArgAspPhelleThrAlaLeuProAlaArgGlyLeuAspHisIleAlaGluAsnIle
                                                                                                                CAGAGAGATTTCATAACTGCTCTGCCAGCTCGGGGATTGGATCATATTGCTGAGAACATT
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                                            520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, cytokine, cell proliferation, cell differentiation, gene therapy,
vaccine, peptide cherapy, stem cell growth factor, haematopolesis,
tissue growth factor; immunomodulatory, cancer, leuksemia,
nervous system disorder; arthritis; inflammation; ss.
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1568 AAGAGGATAGTCAGTGGGGCCTATGATGGAAAAATTAAAGTGTGGGATCTTGTGGCTGCT
                                                                                                                                                                                    TTGGACCCCCGTGCTCCTGCAGGACACTCTGTCTACGGACCCTTGTGGGACCATTCCGGA
                                                                                                         521 ArgValPheArgLeuGlnPheAspGluPheGlnIleValSerSerSerHisAspAspThr
                                                                                                                                                                     541 IleLeulleTrpAspPheLeuAspAspProAlaAlaGlnAlaGluProProArgSerPro
                                           LeuAspProArgAlaProAlaGlyThrLeuCysLeuArgThrLeuValGluHisSerGly
                                                                                                                                      AGAGTITITICGACTACAGTITIGATGAATTCCAGATTGTCAGTAGTTCACATGATGACACA
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Wang
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Wang D, Wang J, Zhang J, Ren F, Chen R,
Yang Y, Wejhrman T, Goodrich R;
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RESULT 12
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tivity, tissue growth factor activity, immunomodulatory activity and tivin/inhibin activity and may be useful in the diagnosis and/or eatment of cancer, leukaemia, nervous system disorders, arthritis and "flammation.
                                                     tte: Records for SEQ ID NO 2110 (AAKS2281), 2111 (AAKS2582) and 3666 (AAM80020) are omitted as the relevant pages from the seguence listing are missing at the time of publication.
                                                                                                                                                                                                                                                                                 AAGACTGAGAATTGTGTGTGGCCAAAAACTTGCCCAATGGCACTTCCAGTATGATTGTG
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                                                                                                              aguence 2285 BP; 646 A; 492 C; 573 G; 574 T; 0 other;
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Matches:
Conservative:
Mismatches:
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qq	907 AAIGCICCCCAACICITITIAIAGAGCACIT	
ò	5 Thrile	SCysArgSer 26
qa	ACAATA	CTGCCGAAGT 10
70	65 GluTh	AspAspGlnLysIleValSerGlyLeu 284
DP DP	27 GAAACA	antagrandededectr 10
δλ	5 ArgAsp	SLysArglleLeuThr 3
qq	87 C	SAGCGAATTCTCACA 1
λ	<b>6</b>	AspGluArgVall1eIleThrGlySer 324
qq	1147 GGCCATACAGGTTCAGTCCTCTGTCTCCAGTA	gargagagagagagarga 1206
ò	325 SerAspSerThrValArgValTrpAspValAs	
qa	1207 regarrecaederadagreredanera	ACAGGIGAATGCIAAACACGIIGATI 1266
Οy	345 HisHisCysGluAlaValLeuHisLeuArgPh	AsnAsnGlyMetMetValThrCysSer 364
qq	1267 CACCAITGIGAAGCAGTICIGCACTIGCGITI	AATAATGGCATGATGATGACCTGCTCC 1326
ΟŊ	365 LysAspArgSerIleAlaValTrpAspMetAl	SerProThrAspileThrLeuArgArg 384
q	1327 AAAGAICGIICCAIIGCIGIAIGGGAIAIGGC	TCCCCAACTGACATTACCCTCCGGAGG 1386
67	385 ValLeuvalGlyHisArgAlaAlaValAsnVa	ValAspPheAspAspLysTyrlleVal 404
qa	1387 GIGCIGGICGGACACCGAGCTGCTGTCAIGI	GTAGACTTTGATGACAAGTACATTGTT 1446
λ0	405 SerAlaSerGlyAspArgThr1leLysValTrpAsnThrSerThrCysGluPheValArg 424	AsnThrSerThrCysGluPheValArg 424
qd	1447 TCTGCATCTGGGGATAGAACTATAAGGTATG	AACACAAGTACTTGTGATTTGTAAGG 1506
òy	425 ThrLeuAsnGlyHisLysArgGlyIleAlaCy	beuGlnTyrArgAspArgLeuValVal 444
qq	1507 ACCTTAATGGACACAAACGAGGCATTGCCTG	TIGCAGIACAGGACAGGCTGGTAGIG
δλ	445 SerGlySerSerAspAsnThrIleArgLeuTr	AspileGluCysGlyAlaCysLeuArg 464
qa	1567 AGIGGCICALCIGACAACACTAICAGAITAIG	sakatakandresikkandritaka 1626
Qy	465 ValLeuGluGlyHisGluGluLeuValArgCy	
qq	1627 GIGITAGAAGGCCATGAGGAATTGGTGCGTTG	ATTCGATTTGATAACAAGAGGATAGTC 1686
ò	485 SerGlyAlaTyrAspGlyLysIleLysValTr	AspLeuValAlaAlaLeuAspProArg 504
QQ	1687 AGTGGGCCTATGATGGAAAATTAAAGTGTG	GANCTIGIGGCIGCTTIGGACCCCCGT 1746
٥y	505 AlaProAlaGlyThrLeuCysLeuArgThrLe	ValGluHisSerGlyArgValPheArg 524
qa	1747 GCTCCTGCAGGACACTCTGTCTACGGACCCT	GIGGAGCATTCCGGAAGAGTTTTTCGA 1806
ογ	525 LeuGlnPheAspGluPheGlnIleValSerSe	SerHisAspAspThrlleLeulleTrp 544
qq	1807 CTACAGTTTGATGAATTCCAGATTGTCAGTAG	TCACATGACACAATCCTCATCTGG 1866
λ'n	545 AspPheLeuAsnAspProAlaAlaGlnAlaGl	
qq	1867 GACTICCTAAATGATCCAGCTGCCCAAGCTGA	CCCCCCCTTCCCCTTCTCGACATAC 1926
δλ	565 ThrTyr1leSerArg 569	
qa	1927 ACCTACATCTCCAGA 1941	
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441 ArgLeuValValSerGlySerSerAspAsnThrIleArgLeuTrpAspIleGluCysGly 460
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                                                                                                                                                                                                                                                             421 CAGAGGGATTTCATAACTGCACTGCCAGCACGGGGTCTGGACCACCACCACATCGCTGAGAACATT
                                                                                                                                                                                                                                                                                                                                       CTGTCATACTTGGACGCCAAGTCACTGTGTGCTGCTGAGCTCGTGTGCAAGGAATGGTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerLeuTrpArgGlyLeuAlaGluArgArgGlyTrpGlyGlnTyrLeuPheLysAsnLys
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      SerMetIleValProLysGlnArgLysLeuSerAlaSerTyrGluLysGluLysGluLeu
                                                                               CysValLysTyrPheGluGlnTrpSerGluSerAspGlnValGluPheValGluHisLeu
                                                                                                              301 TGTGTCAAGTATTTTGAGCAGTGGTCAGAGTCTGATCAAGTGGAATTTTGTAGAACACCTT
                                                                                                                                                         IleSerGlnMetCysHisTyrGlnHisGlyHisIleAsnSerTyrLeuLysProMetLeu
                                                                                                                                                                                                LeuSerTyrLeuAspAlaLysSerLeuCysAlaAlaGluLeuValCysLysGluTrpTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e present invention describes an F-box motif protein of ubiquitin gase SCF complex which promotes the ubiquitination of IkappaB or ta-catenin and is constituted by Skpl protein, cull protein and a mplex (SCF complex) of F-box protein containing F-box motif and WD40 peat motif and has the amino acid sequence of 45 residues (AAB12811) one of two S69 residue sequences (AAB12812, which is mouse ubiquitin gase FWD1 protein) and (AAB12813, which is human beta-transducin peat containing protein (beta-TrCP)). The F-box protein can be used for e game therapy of colon cancer by being recombined to a virus vector. on the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                iquitin ligase SCF complex, P-box protein; ubiquitination; IkappaB; ta-catenin; Skpl; Cull; F-box motif; WD40 repeat motif; PWD1; ne therapy; colon cancer; beta-transducin repeat containing protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetAspProAlaGluAlaValLeuGlnGluLysAlaLeuLysPheMetAsnSerSerGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGGACCCGGCAGAGGCGGTGCTGCAGGAGAAGCGCTTAAGTTTATGAATTCCTCAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AGAGAAGACTGTAATAATGGCGAACCCCCTAGGAAGATAATACCAGAGAAGAATTCACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quence 1707 BP; 467 A; 399 C; 453 G; 388 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which
                                                                                                                use ubiquitin ligase FWD1 protein encoding cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                box protein of ubiquitin ligase SCF compiquitination of IkappaB or beta-catenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-168B-2 (1-569) x AAA73131 (1-1707)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sclosure; Fig 16; 19pp; Japanese.
1707
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                                                                               entry)
  A73131 standard; cDNA;
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PSDB; AAB12812.
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Query Match:
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                                                                                                                                                                                                                                                    1561 AGAGITITICOGCCICCAGITIGATGAATICCAGATIGICAGIAGITCACATGATGACACA
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                                              AlaCysLeuArgValLeuGluGlyHisGluGluLeuValArgCysIleArgPheAspAsn
                                                                                                         LysArgileValSerGlyAlaTyrAspGlyLysIleLysValTrpAspLeuValAlaAla
geting degradation of polypeptide useful for treating cancer and er proliferative disorders, involves conjugating polypeptide with quitin protein ligase or inhibiting ubiquitination using organic pound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lquitin ligase, SCF, F-box protein, targeted degradation,
stabilisation; proteolysis; drug discovery; gene therapy; cancer;
coprotein; Huntington's disease; gene knockout; delivery systems;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= F-box protein FWDlp
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polypeptide in vivo. Targetted degradation is achieved by expressing the target polypeptide and thereby recruiting the target polypeptide and thereby recruiting the target polypeptide to the target polypeptide and thereby recruiting the target polypeptide confined are useful for decreasing or increasing a destabilized polypeptide which is subjected to SCF mediated proteolysis. Begrading any desired protein in a cell is useful for preventing or treating diseases caused by the presence of abnormal amount of the specific polypeptides, for drug discovery and for gene therapy. Diseases treated include cancer, by degradation of concoproteins, Huntington's disease, other proliferative disorders and microbial infections. The method provides a quick and easy alternative to gene knockout technology. The target polypeptide can be degraded at all stages, or a specific stage, of development in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 ATGGACCCGGCAGAGGCGGTGCTGCAGGAGAAAGCGCTTAAGTTTATGAATTCCTCAGAG 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetAspProAlaGluAlaValLeuGlnGluLysAlaLeuLysPheMetAsnSerSerGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2175 BP; 589 A; 528 C; 567 G; 491 T; 0 other;
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F-box proteins are a family of ubiquitin ligases (SCF ubiquitin ases) which can be used for the targetted degradation of a target

im 10; Page 184; 185pp; English.

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AAH89966 standard; cDNA; 3622
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Zhao QA,
                          AAH89966
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                                                                                           HisCysArgSerGluThrSerLysGlyValTyrCysLeuGlnTyrAspAspGlnLysIle
                                                                                                                                           ValSerGlyLeuArgAspAsnThrIleLysIleTrpAspLysAsnThrLeuGluCysLys
                                                                                                                                                                        GTCAGCGGCCTTCGAGACAACACCATCAAGATCTGGGGATAAAAGCACACTGGAATGCAAG
                                                                                                                                                                                                                CGGATTCTCACGGGCCACACGGGCTCCGTCCTGTGTCTGCAGTACGATGAGAGGGTGATC
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                                                               CAAGACATTGAGACAATAGAGTCCAATTGGAGATGTGGGGGGACATAGTTTACAGAGAATC
                                                                                                                  CACTGCCGGAGTGAAACAAGTAAAGGGGTTTACTGTTTACAGTACGACGACCAGAAGATA
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                                       GlnAspileGluThrileGluSerAsnTrpArgCysGlyArgHisSerLeuGlnArgile
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                                                                                                                                                                                                                  Human, bone marrow, antiinflammatory, cytostatic, neuroprotective, antiviral; antibacterial; antifungal; anti-HIV, haemostatic; immunosuppressive; gene therapy, cytokine cell proliferation; cell differentiation modulator; immune disorder; infection; cancer; human immunodeficiency virus; HIV; autoimmune disorder; haemophilia;
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treating e.g. cancer and immune deficiency disorders -
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25-APR-2000; 2000US-0552317.
09-UUL-2000; 2000US-0598042.
19-UUL-2000; 2000US-0620312.
03-APC-2000; 2000US-0633450.
14-SEP-2000; 2000US-063391.
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1 MetAspProAlaGluAlaValLeuGlnGluLysAla-LeuLysPheMet-----

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ATGGACCCGGCCGAGGCGGTGCTGCAAGAAGGCACCTCAAGTTTATGTGCTCTATGCC 1	da Qy	1190 ATCGGATTCCACGGTCAGAGTGTGGGATGTAAATACAGGTGAAATGCTAAACACGTTGAT 1249 344 eHisHisCysGlualaValLevHisLevLATGPREASTASGGJyMetWetValThrCysSe 364
170 CAGGTCTCTGTGGCTGCTCCAGCCTGGCGACAGCATGCCTTCGCTGCGATGCCT 229  17	40 QQ 48	1250 TCACCATTGTGAAGCAGTTCTGCACTTTCAATAATGGCATGATGTGACTGTCTCTGTTC 1309  364 ILVSASpherSerilehlaValTrAspMetAlsSerProThrAsplleThireuargar 384  [
GTATAACCCAGGGACTGGCGCACTCACAGCTTTCCAGAATTCCTCAGAGAGAG	Qy	4 gvalleuvaldiyHisArgAlaAlaValAsnvalValAspPheAspAspLysTyrIleva 40
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GISICATIACCAACAIGGGGGCACAIAAACICGIAICIIAAACCIAIGIIGGGGGGAGAGAIII ST		504 GALAProAlaGlyThrLeuCysLeuArgThrLeuValGluHisSerGlyArgValPheAr 524
CAIRACISCICICCCAGCICGGGGGAIIGGAICAIAIGCCIGAGAACAIICIGICAIAACC WASDAlaLysSerLeuCysAlaAlaGluLeuValCysLysGluTrpTyrArgValThrS-	çç Op	524 gleudinpheAspoluPheGinileValSerSerKisAspAspThrileLeuileTr 544
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YASTALAProProAsnSerPheTyrArgAlaLeuTyrProLysIleIleGlm	AAK AAK ID	JLT 15 51717 AAK51717 standard; CDNA; 2366 BP.
UThrileGluSerAsnTrpArgCysGlyArgHisSerLeuGlnArgIleHisCysArgSe 26	A X E X	K517
rGluthrserLysGlyValTyrCysLeuGlnTyrAspAspGlnLysIleValSerGlyLe 284	DE HU XX XX KW HU KW YA	Human polynucleotide SEQ ID NO 262. Human; cytckine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
284 uargaspasnThrIleLysIleTrpaspLysasnThrLeuGluCysLysArgIleLeuTh 304 	KX KX SO	tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss. Homo sapiens.
304 rGlyHisThrGlySerValLeuCysLeuGlnTyrAspGluArgValllelleThrGlySe 324 	XXXX	WO200157190-A2. 09-AUG-2001.
324 rSerAspSerThrValArgValTrpAspValAsnThrGlyGluMetLeuAsnThrLeuIl 344	XX P XX	05-FEB-2001, 2001WO-US04098.

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Executed for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 M80020) are omitted as the relevant pages from the sequence listing
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to QA, Wang D, Wang J, Zhang J, Ren F, Chen
AJ, Yang Y, Wejhrman T, Goodrich R;
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JUL-2000, 2000US-056005.

JUL-2000, 2000US-055936.

SEP-2000, 2000US-0654936.

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                                                                                                                                       547 GGCACTTCCAGTATGATTGTGCCCAAGCAACGAAACTCTCAGCAAGCTATGAAAAGGAA
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                                 TGTTTAGCAAGCACTGCTATGAAGACTGAGAATTGTGTGGCCAAAACAAAACTTGCCAAT
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completed: October 22, 2003, 15:03:20
e : 422 secs

score: table:

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NAME/KEY: gene
LOCATION: (1)..(1710)
OTHER INFORMATION: Human beta-TrCP1 : F-box containing procein with 7 WD40 repeats;
OTHER INFORMATION: Part of SCF (Skpl/Cullin/F-box) complex E3 ubiquitin ligase; Impl
OTHER INFORMATION: icated in the degradation of b-catenin and IkBa
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Sequence 15, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 2934, Ap
Sequence 190, App
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Sequence 18709, A
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Sequence 7, Application US/10038010

Sequence 7, Application US/10038010

Sequence 7, Application NS/20030040089A1

GENERAL INFORMATION:

APPLICANT: HYBRIGENICS

APPLICANT: Pierre, Legrain

TITLE OF INTERNICE: B4767A

CURRENT APPLICATION NUMBER: US/10/038,010

CURRENT PILING DATE: 2002-07-23

PRIOR APPLICATION NUMBER: US 60/259,377

PRIOR FILING DATE: 2002-07-36

SOFTWARE: Patentin version 3.1

SEQ ID NO 7

LENGTH: 1710
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Sequence 26, 7
Sequence 26, 7
Sequence 24, 7
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Sequence 15,
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                                                                                                                                                             October 22, 2003, 16:26:53; Search time 385 Seconds (without alignments) 3963.493 Million cell updates/sec
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core greater than or equal to the score of the result being printed,
id is derived by analysis of the total score distribution.
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2. /cgn2_6/ptodata/2/pubpna/PCT_NBW PUB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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Sequence 17, Application US/09832161
Sublication No. US2033166587A1
Septence 17, Application No. US2033166587A1
Septence 17, Manning, Anthony M.
APPLICANT: Manning, Anthony M.
APPLICANT: Mait, Sharon
APPLICANT: Ben-Neriah, Yinon
APPLICANT: Ben-Neriah, Yada
APPLICANT: Lavon, Iris
APPLICANT: Lavon, Iris
APPLICANT: Arcon, Avraham
IITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
FILE REFERENCE: 860098.427
CURRENT APPLICATION NUMBER: US/09/832,161
CURRENT FILING DATE: 2001-04-09
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Sequence 1, Application US/10042417

Publication No. US20020123082A1

GENERAL INFORMED.

APPLICANT: Pagano, M.

TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF

TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS

FILE REPREBLUCE: 5914-090-999

CURRENT APPLICATION NUMBER: US/10/042,417
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NT FILING DATE: 2002-01-07
APPLICATION NUMBER: 60/260,179
FILING DATE: 2001-01-5
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                                                       201 SerLeuTrpArgGlyLeuAlaGluArgArgGlyTrpGlyGlnTyrLeuPheLysAsn 219
                                                                        55 GluThrValCysLeuAlaSerThrAlaMetLysThrGluAsnCysValAlaLysThrLys
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Sequence 15, Application US/09764848

Fatent No. US20020077270A1

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PT208

CURRENT FILING DATE:

CURRENT FILING DATE:

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 15

LENGTH: 951
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                                                                                  APPLICANT: BEGALAN, FIGHTS
APPLICANT: BEGALANGUS, Richard
APPLICANT: BLOT, Guillaume
APPLICANT: LASSOT, ITINA
TITLE OF INVENTION: PROTEINS THAT INTERACT WITH BETA TrCP
FILE REFERENCE: B4717A
CURRENT APPLICATION WIMBER: US/10/023,530
CURRENT FILING DATE: 2002-04-22
PRIOR FILING DATE: 2000-12-18
RIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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Matches:
Conservative:
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                 Sequence 1, Application US/10023530 Publication No. US20030007956A1 GENERAL INFORMATION:
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NOAME/KEY: gene
LOCATION: (1)..(657)
OTHER INFORMATION: Beta TrCP
                                                                        APPLICANT: LEGRAIN, Pierre
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lest Local Similarity:
luery Match:
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LENGTH: 657
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R FILING DATE: 2000-09-29
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R FILING DATE: 2000-10-20
R PELING DATE: 2000-11-01
R FILING DATE: 2000-11-01
R APPLICATION NUMBER: 60/225,268
                                                                                                                                      APPLICATION NUMBER: 60/218,290
FILING DATE: 2000-07-14
APPLICATION NUMBER: 60/225,757
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/226,868
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FILING DATE: 2000-07-07
APPLICATION NUMBER: 60/225,267
FILING DATE: 2000-08-14
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APPLICATION NUMBER: 60/241,809
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APPLICATION NUMBER: 60/229,509
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APPLICATION NUMBER: 60/249,299
FILING DATE: 2000-11-17
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APPLICATION WUMBER: 60/251,856
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APPLICATION WUMBER: 60/251,868
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APPLICATION WUMBER: 60/234,997
BILING DATE: 2000-09-25
APPLICATION NUMBER: 60/229,343
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APPLICATION NUMBER: 60/229,345
FILING DATE: 2000-09-01
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FILING DATE: 2000-09-29
APPLICATION NUMBER: 60/237,039
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APPLICATION NUMBER: 60/225,270
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APPLICATION NUMBER: 60/224,519
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APPLICATION NUMBER: 60/220,964
FILING DATE: 2000-07-26
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APPLICATION NUMBER: 60/236,368
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APPLICATION NUMBER: 60/229,344
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APPLICATION NUMBER: 60/229,287
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APPLICATION NUMBER: 60/229,513
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APPLICATION NUMBER: 60/235,834
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APPLICATION NUMBER: 60/234,223
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APPLICATION NUMBER: 60/228,924
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                                     248 GAATTIGIGGAACATCTTATTTCACGAATGTGTCATTATCAGCATGGACATATTAACTCT 307
                                                                                                                                                                                                                                                                                                                                                              175 ValCysLysGluTrpTyrArgValThrSerAspGlyMetLeuTrpLysLysLeuIleGlu 194
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                                                                                                   TyrLeuLysProMetLeuGlnArgAspPheIleThrAlaLeuProAlaArgGlyLeuAsp
                                                                                                                                                                                                                                                                        GTATGTAAAGAATGGCAGCGAGTGATCTCAGAAGGAATGCTTTGGAAGAAGCTGATTGAA
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                                                                                                                                                                        308 TACCTGAAGCCCATGTTGCAGCGGGACTTTATTACCGCTTTACCAGAGCAAGGCTTAGAT
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Sequence 15, Application US/10222020
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT208C2
CURRENT APPLICATION NUMBER: US/10/222,020
CURRENT APPLICATION NUMBER: US/10/16,016
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-04-05
PRIOR PILING DATE: 2000-01-01-17
PRIOR PILING DATE: 2000-01-01-17
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                                                                                                                                   PheMetAsnSerSerGluArgGluAspCysAsnAsnGlyGluProProArgLysIle1le 34
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                   Conservative:
Mismatches:
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Query Match:
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 ValCysLysGluTrpTyrArgValThrSerAspGlyMetLeuTrpLysLysLeuIleGlu
                                 GTATGTAAAGAATGGCAGCGAGTGATCTCAGAAGGAATGCTTTGGAAGAAGCTGATTGAA
                                                                    ArgMetValArgThrAspSerbeuTrpArgGlybeuAlaGluArgArgGlyTrpGlyGln
                                                                                         TACCTGTTTAAAAACAGACCCACAGATGGC-----CCTCCAAATTCATTTTATAGGTCA
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TITLE OF INVENTION: Nucleic Acids, Froteins, and FILE REFERENCE: PIZORCI
CURRENT APPLICATION NUMBER: US/10/116,016
CURRENT FILING DATE: 2002-04-05
Prior Application removed - See File Wrapper or Number OF Seg ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AsnThrGlyGluMetLeuAsnThrLeuile 344
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FRATURE:
NAME/KEY: misc feature
LOCATION: (883)
O'THER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (913)
O'THER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (931)
O'THER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (935)
O'THER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (935)
LOCATION: (941)
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S-10-116-016-15
Sequence 15, Application US/10116016
Publication No. US20030054379A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Sequence 20, Application US/09213808A

Patent No. US20020164683AI

GENERAL INFORMATION:

APPLICANT: Li, Jinhe

APPLICANT: Pharmacia & Upjohn Company

TITLE OF INVENTION: Haman Sel-10 Polypeptides and Polymucleotides that

TITLE OF INVENTION: Encode Them

FILE REPERENCE: 6142

CURRENT APPLICATION NUMBER: US/09/213,888A

CURRENT FILING DATE: 1998-12-17

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 20

LENGTH: 1881
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Matches:
Conservative:
Mismatches:
Indels:
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CTHER INFORMATION:
US-09-213-888-20
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US-09-213-888-20
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                                                                                                  Sequence 2778, Application US/09864761
Sequence 2778, Application US/09864761
GEREEAL INFORMATION PERM, Sharran G.
APPLICANT, Perm, Sharran G.
APPLICANT, Perm, Sharran G.
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APPLICANT, Perm, Sharran G.
APPLICANT, Perm, Sharran G.
TITLE OF INVENTION: HINAM TERRESION ANALYSIS BY MICHARAY
FILE BETERNER: Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded. Accorded.
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.6
OTHER INFORMATION: EXPRESSED IN HBL4, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN BLA4, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN BLA7, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BAIN, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
                          900 ACACCGGTGAAGNTCTTAACACATTGATC 929
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	348 GluhlaValLeuHisLeuArgPheAsnAsnGlyMetMetValThrCysSerlysAspArg 367  1141 TCCACTGTGCGTTGTATGCATCTTCATGAAAAAGGGTTGTTAGCGGTTCTCGAGATGCC 1200  368 SerlleAlaValTrpAspMetAlaSerProThrAspIleThrLeuArgArgValLeuVal 387  :::::           ::: ::          ::: ::	388 GlyHisArgAlaAlaValAsnValValAspPheAspAspLysTyrIleValSerAlaSer 407	428 GlyHisLysArgGlyIleAlaCysLeuGlnTyrArgAspArgLeuValValSerGlySer 447 :::	468 GlyHisGludluLeuValArgCysIleArgPheAspAsnLysArgIleValSerGlyAla 487	GlyThr Leugln       TTACAG	Oy 545 Asp 545	GENERAL INFORMATION: APPLICANT: Ourney, Mark E. APPLICANT: Li, Jinhe APPLICANT: Pauley, Adele M. APPLICANT: Pharmacia & Upjohn Company TITLE OF INVENTION: Human Sel-10 Folypeptides and Polynucleotides that TITLE OF INVENTION: Encode Them FILE REFERENCE: 642	VERENT FILIALION NUMBER: US/US/328,87/A URRENT FILIAL GATUS, 1999-06-09 URRENT FILIAL DATE: 1999-06-09 UMBER OF SEQ ID NOS: 27 OFTWARE: Patentin Ver. 2.0 OFTWARE: Patentin Ver. 2.0 OFTWARE: Patentin Ver. 2.0 TRES DNA ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: 6 myc tagged
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core: 644.50 Matches: 169 ercent Similarity: 48.48% Conservative: 103 est Local Similarity: 30.12% Mismatches: 222 uery Match: 21.24% Indels: 67 B: 10 Gaps: 15	8 LeuGlnGluLysAlaLeuLysPheMetAsnSerSerGluArgGluAspCysAsnAsnGly		337 ACAAGTACCACTGGGGTTGTACCATGTTCAGCAACACCAACACTTTTGGGGACCTCAGA 75 LeualaasnGlyThrSerSerMetlleValProlysGlnArgLysLeuSerAlaSerTyr	113 GlnValGluPheValGluHisLeuIleSerGlnMetCysHisTyrGlnHisGlyHisIle 132  113 GlnValGluPheValGluHisLeuIleSerGlnMetCysHisTyrGlnHisGlyHisIle 132  113 GlnValGluPheValGluHisLeuIleSerGlnMetCysHisTyrGlnHisGlyHisIle 132  133 AshIfGCTTGCTTTAGATGAACTCATTGATAGTTGTGAACCAACACAAGAAAAATATTG 561  133 AshSerTyrLeuLysProMetLeuGlnArgAspPheIleThrAlaleuProAlaArgGly 152  152 AnggaagaagaaCcCagnmacaagaaCcCagnmacaagaaCcCCCCagnaagaagaaCcCCCagnaagaagaaCcCCCagnaagaaCcCCCCCCCCCC	153 LeuAspHisTleAlaGluAsnIleLeuSerTyrLeuAspAlaLysSerLeuCysAlaAla 153 LeuAspHisTleAlaGluAsnIleLeuSerTyrLeuAspAlaLysSerLeuCysAlaAla 153AAAGAGTTGGCACTCTATGTGCTTTCTGGAACCCAAAGACCTGCTACAAGCA 173 GluLeuValCysLysGluTrpTyrAragGTTATGGTASpGlyMetLeuTrpLysLysLysEuu 173 GluLeuValCySLyGGTTTGGGTAATTTGGCTGAAGAGAAA	193   IleGluArgMetValArgThrAspSerLeuTrpArgGlyLeuAlaGlu 208	ProAssSerPheTyrArgAlaLeuTyrProLysIleIleGlnAsplleGluThrIleGlu	268 LysGlyValTyrCysLeuGlnTyrAspAspGlnLysIleValSerGlyLeuArgAspAsn 287 :::            :::

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961 ACTTTAAAAGTTTGGTCAGCAGTCACAGGCAATGTCTGAGAACATTAGTGGGAACATACA 1020
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      ThrileLysileTrpAspLysAsnThrLeuGluCysLysArgIleLeuThrGlyHisThr
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APPLICANT: Strohmaier, Heimo
APPLICANT: Strohmaier, Heimo
APPLICANT: Spruck, Charles
APPLICANT: Spruck, Charles
TITLE OF INVENTION: HCDC4 MODULATES CYCLIN E DEGRADATION
FILE REPERENCE: TSN 179.2
CURRENT APPLICATION NUMBER: US/10/245,618
CURRENT FILING DATE: 2002-09.16
PRIOR FILING DATE: 2002-09.16
PRIOR FILING DATE: 2002-08-15
PRIOR FILING DATE: 2002-08-15
PRIOR FILING DATE: 2001-09-14
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Publication No. US20030143582A1
GENERAL INFORMATION:
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277 CATGGTTCTGAGGTCCGCTCTTTTCTTTGGAAAGAAACCATGCAAAGTCTCAGAATAT 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         397 GCAGCCAATGGCCAAGGG-------CAACAACGACGCCGAATTACATCTGTC 441
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CAGCCACCTACAGGCTCCAGGAATGCTAAAATGTTTCAGAGCTGGAGTGGACCAGAG
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Matches:
Conservative:
Mismatches:
Indels:
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OTHER INFORMATION: homo sapiens
S-09-328-877A-20
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    AsnThrlleLys1leTrpAspLysAsnThrLeuGluCysLysArglleLeuThrGlyHis
                                                                                                                                                                                760 ACAGGIGGAGIAIGGICAICACAAAIGAGAGACAACAICAICAIIAGIGGAICIACAGAI
                                                                                                                                                                                                                                                                                                347 CysGluAlaValLeuHisLeuArgPheAsnAsnGlyMetMetValThrCysSerLysAsp
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                                                                                                     700 AACACTITAAAAGITIGGICAGCAGICACAGGCAAAIGICIGAGAACAITAGIGGACAT
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APPLICANT: Strohmaier, Holos
TITLE OF INVENTION: HOCG4 MODULATES CYCLIN E DEGRADATION
FILE REFERENCE: TSR1 779.2
FURE REFERENCE: TSR1 779.2
CURRENT APPLICATION NUMBER: US/10/245,618
PRIOR APPLICATION NUMBER: US 60/404,116
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NUMBER, OF SEQ ID NOS: 48
SEQ SOFTWARE: RastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 1620
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APPLICANT: Strohmaier, Heimo
APPLICANT: Spruck, Charles
APPLICANT: Sangfelt, Olle
TITLE OF INVENTON: HCDC4 MODULATES CYCLIN E DEGRADATION
FILE REFERENCE: TSRI 779.2
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Publication No. US20030143582A1
GENERAL INFORMATION:
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Conservative:
Mismatches:
Indels:
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PRIOR FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/322,947
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCAAGAGAAAAA-----
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                                                                                                                                                                               OTHER INFORMATION: Synthesized JS-10-245-618-7
                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
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30.81%
21.09%
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Best Local Similarity:
Query Match:
JB;
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AACACTTTAAAAGTTTGGTCAGCAGTCACAGCCAAATGTCTGAGAACATTAGTCGGACAT
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----CACAGAATT
                                   GluSerAsnTrpArgCysGlyArgHisSerLeuGlnArgIleHisCysArgSerGluThr
                                                                    730 GATACTAACTGGAGGCGAGGAGCACTCAAATCTCCTAAGGTG----CTGAAAGGACATGAT
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Sequence 5, Application US/10245618

Publication No. US20030143582A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven

APPLICANT: Strohmaier, Heimo
594 CCATGGAAAAGTGCATAC-
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388 GAGAAATIGCTITGCTITAGATGAACTCATIGATAGTIGTGAACCAACACAAGTAAAAACAT 447
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             CURRENT FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US 60/404,116
PRIOR FILING DATE: 2002-08-15
PRIOR PELICATION NUMBER: US 60/322,947
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 48
SOOTWARE: Patcseq for Windows Version 4.0
LENGTH: 1770
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CURRENT APPLICATION NUMBER: US/10/245,618
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961 AACACTITAAAAGTTTGGTCAGCAGTCACAGGCAAATGTCTGAGAACATTAGTGGGACAT 1020
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 GTAATAAAACCAGGTTTCATACACAGT
                                                                                    247 GluSerAsnTrpArgCysGlyArgHisSerLeuGlnArg1leHisCysArgSerGluThr
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                             ProProAsnSerPheTyrArgAlaLeuTyrProLysIleIleGlnAspIleGluThrIle
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Matches:
Conservative:
Mismatches:
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         APPLICANT: Sangfelt, Olle
TITLE OF INVENTION: HCDC4 MODULATES CYCLIN E I
FILE REPERENCE: TSR 179.2
CURRENT APPLICATION NUMBER: US/10/245,618
CURRENT FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-09-16
PRIOR FILING DATE: 2002-08-15
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FaeLSEQ for Windows Version 4.0
SEQ ID NO 5
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LOCATION: (1)
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us-09-601-168b-2.rnpb

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APPLICATION NUMBER: US/08/89,578
FILING DATE: 24-UUL.1997
CLASSIFICATION: 435
ATTORNEY/AGANT INPORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 08,555
TELECOMMUNICATION INFORMATION:
TELECHHONE: (212) 278-9400
US-09-092-508-15
US-08-48-115-15
US-08-646-715-17
US-08-69-715-17
US-09-690-364-10
US-09-063-743-2
US-09-590-540-2
US-09-500-540-2
US-09-500-540-2
US-09-620-312D-615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08899578
Patent No. 6087153
GENERAL INFORMATION:
APPLICANT: Hubbard, Iva
APPLICANT: Hubbard, E. Jane
TITLE OF INVENTION: SEL-10 AND USES THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                       US-09-060-836-2
US-09-184-445-2
US-09-620-312D-222
US-08-965-600-2
US-09-489-506-2
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US-08-477-346-19
US-08-473-089-19
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US-09-032-372-6
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ZIP: 10036
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 1:
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MODEL-frame+promedel-DEV=xlp

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FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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Sequence 730, App
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Sequence 4, Appli
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Sequence 21, Appli
                                                                                                        October 22, 2003, 14:52:38 ; Search time 100 Seconds (without alignments) 2511.470 Million cell updates/sec
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6: /cgn2_6/prodata/1/ina/PcTUS_COMB.seq:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                              - nucleic search, using frame_plus_p2n model
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US-08-911-716-8

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US-08-61-715-730

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US-08-08-508-1

US-09-435-115-1

US-09-438-310-1

US-09-690-364-21
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Maximum Match 100%
Listing first 45 summaries
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                                    GlnTyrAspGlu-----ArgVallleIleThrGlySerSerAspSerThrValArgVal
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APPLICANT: Ryazanov, Alexey G.
APPLICANT: Hait, William N.
APPLICANT: Hait, William N.
APPLICANT: Pavur, Karen S.
TITLE OF INVENTION: ELONGATION FACTOR-2 KINASE (EF-2 KINASE)
TITLE OF INVENTION: AND METHODS OF USE THEREFOR NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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STATE: New Jersey
COUNTRY: USA
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MOLECULE TYPE: DNA (genomic)
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JS-08-899-578-1
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      209 ArgArgGlyTrpGlyGlnTyrLeuPheLysAsnLysProProAspGlyAsnAlaProPro 228
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APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: TSUJIMOTO, MASAFUMI
APPLICANT: INCUE, KEIZO
APPLICANT: ARAI, HIROTUKI
TITLE OF INVENTION: OXIDIZED PHOPHOLIPID DEGRADING ENZYME
TITLE OF INVENTION: AND GENE THEREOF
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
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Patent No. S849557
GENERAL INFORMATION:
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-09-601-168B-2 (1-569) x US-08-914-999-7 (1-2237)
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/914,999
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFISENCE/FOCKET NUMBER: 601-1-078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                    Dictyostelium discoideum
                                                                                                                                                          601-1-078
                                                                                                                                                                                                                 TELEFAX: 201.343-1684
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2237 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.59e-35
392.00
41.18%
24.14%
                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
ORGANISM: Dic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                     967 GAATTAGATAAGAAATATGCTGGTCTTTTGGAAAAAAATGG------ACATCTGTT 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTACGTCGGGTGGACCTCTTGGTCAG-----AAAAGAGACCCAAAAGAATGGATT 1128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeulleHisHisCysGluAlaValLeuHisLeuArgPhe----AsnAsnGlyMetMet 360
                                                                                                                                                                                                                                                                                               996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlyHisThrGlySerValLeuCysLeuGlnTyrAspGlu-----ArgValIleIleThr 322
                                     -IleAsnSerTyrLeuLysProMet 139
                                                                                                             LeuGlnArgAspPhelleThrAlaLeuProAlaArgGlyLeuAspHisIleAlaGluAsn 159
                                                                                                                                      GTGCTGTCCCAGAGACAACGAGATGAACTAAATCGAGCTATAGCAGATTATCTTCGTTCA 906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlySerSerAspSerThrValArgValTrpAspValAsnThrGlyGluMetLeuAsnThr
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                                                                                                                                                                                                                                                                                   265 GluThrSerLysGlyValTyrCysLeuGlnTyrAspAspGlnLyslleValSerGlyLeu
--CTGGTTACACGTTGGATTCACTTGTGAAAGAATCATTTTCCCCTGCGTGAA
                                                                        736 AGCCACTTAGTGGCTTATTAATTATAAATCCAGGGGTTGCAAAGCTTTTTG-----ATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 GAGCGCCTGAC-------CCCACCGAACCATCCGCAGCATCCACCACCAA
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                                   1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPILICATION NUMBER: US/08/283,917
FILING DATE: 03-AUG-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
SPIVAK, MCCLELLAND, MAIER DT. P. C.
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                                                                                                                                                                                                                                                                                                                                                                                                          2292-030-0
                                                                                                                                                                                                                                                       FILING DATE: 03-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 209943/1993
FILING DATE: 03-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 NAME: Oblon, No. 584955man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2292-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-220
TELEFAX: (703) 413-220
TELEX: 24,618
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 2085 base pairs
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365.50
38.83%
22.84%
12.05%
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844..2073
 ADDRESSEE: OBLON, SI
ADDRESSEE: NEUSTADT
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                                                      Arlington
                                                                            Virginia
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Best Local Similarity:
                                                                                             U.S.A
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Pred. No.:
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US-08-283-917-8
                                                      CITY: Arl
STATE: Vi
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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us-09-601-168b-2.rni

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967 GAATTAGATAAGAAATATGCTGGTCTTTTGGAAAAAAAAGG------ACATCTGTT 1017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     790 TICCAGAGGAGGCATAACCACTATA---TCGAATAAGCTTGATATTACAGCCAAAATG 846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----CCCACCGAACCATCCGCAGCATCCACCCACCAA 507
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                              4.83e-32
365.50
38.83%
22.84%
LENGTH: 2085 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                          ORGANISM: Bos taurus
                                                                                                                                                                                , LOCATION: 844..2073
US-08-961-716-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            463 GAGCGGCCTGAC
                                                            TOPOLOGY: unknown
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                495 TrpAspLeuValAlaAlaLeuAspProArgAlaProAlaGlyThrLeuCysLeuArgThr 514
                         441
                                                                                                                                                                                  457 IleGluCysGlyAlaCysLeuArgValLeuGluGlyHisGluGluLeuValArgCysIle 476
                                                                                                                                                                                                                                                                  477 ArgPheAspAsn-----LysArgIleValSerGlyAlaTyrAspGlyLysIleLysVal 494
                                                                                                                                                                                                                                                                                                                                                                                                                               515 LeuValGluHisSerGlyArgValPheArgLeuGlnPheAspGluPhe-----GlnIle 532
                                                                                                     -LeuValValSerGlySerSerAspAsnThrIleArgLeuTrpAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence B, Application US/08961716
Patent No. 5880272
GENERAL INFORMATION:
APPLICANT: ADACH!, HIDEKI
APPLICANT: INOUE, KEIZO
APPLICANT: INOUE, KEIZO
APPLICANT: ARAI, HIROYUKI
TITLE OF INVENTION: OXIDIZED PHOPHOLIPID DEGRADING ENZYME
TITLE OF INVENTION: AND GENE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..., "GCLELLAND, MAIER & ..., "GCLELLAND, MAIER & CITY: 1755 S. Jefferson Davis Highway, Suite 400 STATE: Virginia CUNTRY: U.S.A.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,716
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APPLICATION NUMBER: US 08/283,917
FILING DATE: 03-AUG-1994
APPLICATION NUMBER: JP 209943/1993
FILING DATE: 03-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5880272man F.
REGISTRATION NUMBER: 24,618
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECHANTINICANTON INPORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-220
TELEFAX: (703) 413-220
TELEFAX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                     439 ArgAspArg------
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50.00%
30.15%
11.11%
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STRANDEDNESS: double
                                                                                                                                                                                                    CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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                                              GENERAL INFORMATION:
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Best Local Similarity:
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Pred. No.:
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   225 AsnAlaProProAsnSerPheTyrArgAlaLeuTyrProLysIleIleGlnAspIleGlu
                                                                                                                 265 GluThrSerLysGlyValTyrCysLeuGlnTyrAspAspGlnLysIleValSerGlyLeu
                                                                                                                                   323 GlySerSerAspSerThrValArgValTrpAspValAsnThrGlyGluMetLeuAsnThr
                                                                                                                                                                                                                                                                                                                                                                 361 ValThrCysSerLysAspArgSerIleAlaValTrpAspMetAlaSerProThrAspIle
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                                                         245 ThrileGluSerAsnTrpArgCysGlyArgHisSerLeuGlnArgIleHisCysArgSer
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                            1129 CCCCGTCCACCAGAAAATATGCATTGAGTGGTCAT-
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APPLICANT: Ryazanov, Alexey G.
APPLICANT: Hair, William N.
APPLICANT: Hair, William N.
APPLICANT: Bavur, Karen S.
TITLE OF INVENTION: BLONGATION FACTOR-2 KINASE (BF-2 KINASE)
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Usablessees
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79
79
52
103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIPICATION: 435
ATTORNEY/AGBNT INFORMATION:
NAME: Jackson Beg., David A.
REGISTRATION NUMBER: 26,742
REPERENCE/DOCKET NUMBER: 601-1-078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Dictyostelium discoideum US-08-914-999-5
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TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3465 base pairs
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                              334.50
37.50%
23.31%
11.03%
                                                                                  ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (147)..(1511)
US-09-620-312D-730
SEQ ID NO 730
LENGTH: 1909
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                         Alignment Scores:
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3301 GATCTCGATACACTTGAATGTGTTTACACCATTCCAAAATCTCATTCTTTGGGTGTAAAA 3360
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                                                                                                                       TTTAAAGAAATTAAATCATTTGAGGGTGTTCATACAAGTACATTAAAACATTGGCTTTG 3009
                                                                                                                                                                                                                                               376 SerProThrAspIleThrLeuArgArgValLeuValGlyHisArgAlaAlaValAsnVal 395
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GluArgValIlelleThrGlySerSerAspSerThrValArgValTrpAspValAsnThr 336
                                                                                  GlyGluMetLeuAsnThrLeuIleHis---HisCysGluAlaValLeuHisLeuArgPhe 355
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TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/620,312D CURRENT FILING DATE: 2000-07-19 PRIOR APPLICATION NUMBER: 09/552,317 PRIOR APPLICATION NUMBER: 09/488,725 PRIOR APPLICATION NUMBER: 09/488,725 PRIOR APPLICATION NUMBER: 09/488,725 PRIOR FILING DATE: 2000-01-21 NUMBER OF SEQ ID NOS: 1105 SOFTWARE: pt_FL_genes Version 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 730, Application US/09620312D
Patent No. 656662
GENERAL INFORMATION:
APPLICANT: Liu', Chenghua
APPLICANT: Liu', Chenghua
APPLICANT: Liu', Chenghua
APPLICANT: Rei, Feiyan
APPLICANT: Rei, Feiyan
APPLICANT: Rei, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Well, Aidong J.
APPLICANT: Ang, Yonghong
APPLICANT: Ang, Yonghong
APPLICANT: Ang, Jian-Rui
APPLICANT: Ang, Jian-Rui
APPLICANT: Ang, Jian-Rui
APPLICANT: May, Jian-Rui
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APPLICANT: May, Jian-Rui
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John Tillinghast
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APPLICANT:
APPLICANT:
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CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Osman, Richard A REGISTRATION NUMBER: 36,627 REFERENCE/DOCKET NUMBER: 4-57650-2/AJT/RAO FELECOMINICATION INFORMATION: TELEPHONE: (415) 781-1989 FELEPHONE: (415) 781-1989 FELEPHONE: (415) 781-1989 FELEX: 910 27729 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHRACATERISTICS: LENGTH: 2359 base pairs TYPE: nucleic acid STRANDENESS: double TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE: MAME/KEY: CDS LOCATION: 492160 US-08-188-582-4	Alignment Scores: Pred. No.: Pred. No.: Score: Score: Percent Similarity: Percent Similarity: Percent Similarity: Percent Similarity: 10.15\$ Rismatches: 117 Bast Local Similarity: 10.15\$ Rismatches: 117 Bast Local Similarity: 10.15\$ Rismatches: 117 Bast Local Similarity: 10.15\$ Rismatches: 117 Bast Local Similarity: 10.15\$ Rismatches: 117 Bast Local Similarity: 10.15\$ Rismatches: 117 Bast Local Similarity: 10.15\$ Rismatches: 117 Bast Local Similarity: 118 Bast Local Similarit	Db 513 CAGTGGACTAAGGGCCAAAGAATTCATTGAGAAGTACAAATGCGA 563  Oy 126HisTyrGlnHisGlyHisIleAsnSerTyrLeuLysPro 138  Est TCTCGACGGCTACTACATAGAGGGTCTTTTCAACCTGCTGTGTAAGCCCGAGGA 623  Oy 139 -MetLeuGlnArgAspPheIleThrAlaLeuPro	150 aArgClyLeuAspHis:lieAlachaschaschaschaschaschaschaschaschascha	912 GGLYTrpGlyGlnTyrLeuPhe
Db   1708   17	470 GluGlu	Oy 519 SerGlyArgValPheArgLeuGlnPheAspGluPheGlnIleValSer 534	NESULT 7 10S-08 188-582-4 10S-08 188-582-4 10S-08 188-582-4 10S-08 188-582 10S-08 188-10 188-	APPLICANT TITLE OF TITLE OF TITLE OF CORRESPON ADDRESS STREET: CITY: STATE: STATE: COUNTRY ZIP: COMPUTEN MEDIUM MEDIUM COMPUTEN COMPUTEN COMPUTEN COMPUTEN COMPUTEN APPLICAN

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684 CAGGGACTCGCACTCTCTGAAGGGACACATTCAG-----GATCGCCGGCAGGAAGT 737
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                                                                                                                                                                              USE
APPLICANT: Dynlact, Brian D.
APPLICANT: Hoey, Timothy
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Naoko
APPLICANT: Wang, Edith
APPLICANT: Weinzierl, Robert O. J.
TITLE OF INVENTION: TATA-BINDING PROTBIN ASSOCIATED FACTORS,
TITLE OF INVENTION: UNCLEIC ACIDS ENCODING TAFS AND METHODS OF NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2359
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1193
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,715
FILING DATE: 09-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/188,582
FILING DATE: 28-UAN-1994
ATTORNEY AGENT INFORMATION:
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPRAX: (415) 398-3249
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                                                                                                                                                                                                                                                                                                                                                                  ZIP: 9411-4187
COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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308.00
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STRANDEDNESS: double
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LOCATION: 49..2160
US-08-646-715-4
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     ----CTTAAGGCTCTCAGGGAAGCCAGCAAGCGTTTAGCCCTCAGCAAGGATCA 1139
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                                                                                                      1140 ACTGCCCTCTGCCGTCTTCTACACGGTGCTTAATTCCCATCAGGGCGTAACCTGTGCCGA
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Patent No. 5637686
GENERAL INPORMATION:
APPLICANT: Tjian, Robert
APPLICANT: Comai, Lucio
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2 AspProAlaGluAlaValLeuGlnGluLysAlaLeuLysPheMerAsnSerSerGluArg 21 :::	22 GluaspCysasnasnGlyGluProProArg	34 IleProgluLysAsnSerLeuArg	42 GlnThrTyrAsnSerCysAlaArgLeuCysLeuAsnGlnGlu-ThrValCysLeuAlaSe 61	61 rThrAlaMetLysThrGluAsnCysValAlaLysThrLysLeuAlaAsnGlyThrSerSe 81 :	81 rMetlleValProLysGlnArgLysLeuSerAlaSerTyrGluLysGluLysGluLeuCy 101	101 sValLysTyrPheGluGlnTrpSerGluSerAspGlnValGluPheValGl 118	118 UHisLeulleSerGlnMetCysHisTyrGlnHisGlyHisIleAsnSerTyrLeuLysPr 138	138 OMETLEUGInArgAspPheIleThrAlaLeuProAlaArgGlyLeuAspHisIleAlaGl 158	158 UASNIIeLeuSerTyrLeuAspAlaLys	168	181	190 sLysleulleGluargMetValargThraspserleuTrpar 204	204 gGlyLeuAlaGluArgArgGlyTrpGlyGlnTyrLeuPheLysAsnLysProProAspGl 224 2398 2398	224 yASDAlaProProASDSerPheTyrArgAlaLeuTyrProLysIleIleGlDASpIleGl 244 2399GAGGATGCTGCTGCTTTTCTGAGGATGGTCA 2427	244 uThrileGluSerAsnTrpArgCysGlyArgHisSerLeuGlnArglleHisCysArgSe 264 :::::::::::::::::::::::::::::::::::	264 rGluThrSerLys	274 nTyrAspaspGlnLysIleValSerGlyLeuArgAspasnThrIleLysIleTr 292 :::	292 pAspLysAsnThrLeuGluCysLysArgIleLeuThrGlyHisThrGlySerValLeuCy 312
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Oy 491 sileLysValTrpAspLeuValAlaAlaLeuAspProArgAlaProAlaGlyThrLeuCy 511	5015 AG.CAAGGIANIGARIANIANIANIGAAGAANAAAAAAAAAAAA	529 uPheGlnIleValSerSerSerHisAspAspThrIleLeuIleTrpAspPhe 546 53706 TACCAGTTTTCATCACTGCTACAGAGTGCAAAACTGCAAAACTGCAAAACTTGCAAAATTTT 3757	SULT 10 09-435-115-1	S/OS455115		. 6346607west Center, 90 is	; COMPUTER READABLE FORM: ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Diskette ; COMPUTER: IBM Compatible	; OPERATING SYSTEM: DOS ; SOFTWARE: FastSEQ for Windows Version 2.0 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/09/435,115	FILING DATE: CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/092,508	258	) NAME: RECUELDERGEK, D.D. Denise M ; REGISTRATION NUMBER: 33,924 ; REFERENCE/DOCKET NUMBER: 11669.6USU1 ; TELECOMMINICATION INFORMATION:	TELEFACNE: 812-332-9300   TELEX: 612-332-9081   TELEX:		; TOPOLOGY: linear ; MOLECULE TYPE: cDNA ; FEATURE: ; NAME/KEY: Coding Sequence		Scores: 1.59e-23 Length: 299.50 Matches: 1.14 Conservati	IILY: 20.32* Mishacches: 9.87\$ Indels: 4 Gaps:	US-09-601-168B-2 (1-569) x US-09-435-115-1 (1-7042)

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APPLICANT: Alnemati, Emad S.
TITLE OF INVENTION: TRUNCATED APAF-1 AND METHODS OF UTILE OF INVENTION: TRUNCATED APAF-1 AND METHODS OF UTILE OF INVENTION: TRUNCATED APAF-1 AND METHODS OF UTILE DEPERBNCE: 480140,438
CURRENT APPLICATION UNDHER: US/09/098,310
CURRENT PALING DATE: 1998-06-16
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PastSEQ for Windows Version 3.0
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Patent No. 6403765
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CCTCAAACTTTGGGATTTGAATCAAAAAGAATGTCGAAAATACCATGTTTGGTCATACAAA 2775
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                                                                                                                        2956 TTCGTGGTCTGCTGATGGTGCAAGGATAATGGTGGCAGCAAAAAATAAAATCTTTTTGTG 3015
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                                                                                      -----ValileIleThrGlySerSerAspSerTh 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GlyHisArgAlaAlaValAsnVa
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                                                                                   sLeuGlnTyrAspGluArg--
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Qy         413 sValTrpAsnThr	Oy 420 sGluPh 422	Qy         434 aCysLeuGlnTyrargAspargLeuValValSerGlySerSerAspasnThr11 452           11   1   1   1   1   1   1   1   1   1	Oy 472 uValArgCysileArgPheAspAsnLysArgileValSerGlyAlaTyrAspGlyLy 491	Db 3613 AGTGAAGGATGTTATTATTATTGGAAATAAAGAA	Oy 529 uPhedInIleValSerSerSerBerBerBerDrileLeulleTrpAspPhe 546 :::	RESULT 12 0.05-69-364-21 1.5-05-69-364-21 1.5-05-69-364-21 1.5-05-69-364-21 1.5-05-69-364-35 1.5-05-69-364-35 1.5-05-69-364-30 1.5-05-69-364-364-30 1.5-05-69-3	; SEQ_1D NO_21 ; TYPE: DNA ; ORGANISM: HOMO Sapiens ; FEATURE: ; LOCATION: (578)(4162) US-09-690-364-21	Alignment Scores: Pred. No.: Pred. No.: Score: Score: Percent Similarity: 23.77% Conservative: 102 Best Local Similarity: 20.32% Mismatches: 195 Query Match: 4 Gaps: 34
158 uAsnIleLeuSerTyrLeuAspAlaLys	SLysLeuileGluArgMetValArgThrAspSerLeuTrpAr	yAsnAlaProProAsnSerPheTyrArgAlaLeuTyrProLysIleIleGlnAspIleGl 2	rGluThrSerLysGlyvalTyrCysLeuGl 	2536 ATTCTATAGACTAGACTAGACAACAACTAGACAAGATAAAAAAGTGAAGATTTG 2 292 PASpLysAsnThrLeuGluCysLysArgIleLeuThrGlyHisThrGlyGerValleuCy 3 2596 GAATTCTATGACTAGACTAGACAACAACAACAACAACAACAACAACAACAAAAAAGTAAAAAAAA	312 sLeuGlnTyrAspGluArgvalllelleThrGlySerSerAspSerTh 2656 CTGCCATTTCACCAACAGTAGTCATCATCTTCTTAGCCACTGGGTCAAATGACTGTT	Oy 328 rValArgValTrpAspValAsnThrGlyGluMetLeuAsnThrLeu11eHisHisCysGl 348 :::::::::      ::       ::         ::	Qy         38.3         9	Qy 388

	Oy 292 pAspLysAsnThrLeuGluCysLysArglleLeuThrGlyHisThrGlySerValLeuCy 312	2656 CTGCCATTTCACCAACAGTAGTCATCATCTTCTCTTAGCCACTGGGTCAAGTGACTGCTT 27 328 rValArgValTrpAspValAsnThrGlyGluMetLeuAsnThrLeuIleHisHisCysGl 34	Db 2716 CCTCAAACTGGGATTGGATCGAAAAGAATGTCGAAATACCATGTTTGGTCTTAGAAA 2775 Qy 348 UAlavalLeuHisLeuArgPheAsnAsnGlyMetMetValThxCysSerLysAs 366 Db 2776 TTCAGTCAATCACTGCAAATTTTCACCAGATGATAAAGCTTTTGGCTAGTTGTTCAGCTGA 2835	366 pargserilealavaltrpaspMetalaSerProThrAspIleThrLeuar	UY 38.9 GITTELECTARANTITGGAGGACCCTCAAGAGGATAIGGAAGTGATAGTGAAGTGTIG 2955  QY 384AKGVALLeUVAL387	Db 2956 TICGIGGICTGCTGAAGGATAATGGTGGCACAAAAAATAAAAT		413 sValtpasnthr	3196 TGTTGTGTTTCAAGAAAATGAAGTGATGGTCCTTGCAGTTGACCATATAAGACGTCTGCA	OY 418SELINEY 420  DD 3256 ACTCATTAATGGAAGAACAGGTCAGATTGATTATCTGACTGA	3316 TTGCTTAAGTCCACATCTTCAGTACATTGCATTTGGAGATGAAAATGGAGCCATTGAGAT	<pre>Qy 422 eValArgThrLeuAsnGly</pre>	434 aCysLeuGlnTyrArgAspArgLeuValValSerGlySerSerAspAsnThrill	452 eArgleuTrpAspIleGluCysGlyAlaCysLeuArgValLeuGluGlyHisGluGluLe  -:::::    :::::::    ::::     :::	472 uValArgCysIleArgPheAspAshLysArgIleValSerGlyAlaTyrAspGlyLy	Oy 491 slleLygValTrpAspLeuValAlaAlaLeuAspProArgAlaProAlaGlyThrLeuCy 511 :::           :::::::::::::::::::::
01-168B-2 (1-569) x US-09-690-364-21 (1-7042)	2 AspProAlaGluAlaValLeuGlnGluLysAlaLeuLysPheMetAsnSerSerGluArg 21 :::	GluAspCysAsnAsnGlyGluProProArg	ILEKTÖĞINUŞASINEFLEGERĞ	1937 CAGAGATATCACCAGCAGCATACTCTTTCACCAGATCAGGAAGACTGTATGTA	rMetileValProLysGlnArgLysLeuSerAlaSerTyrGluLysGluLysGluLeuCy	svallyslyfriedlu	2104 TCATCTGATTCATGAATTTGTGGAATACAGACAT	158 uAsnileLeuSerTyrLeuAspAlaLys	168 SerleucysAlaAlaGluLeuValCysLysGluTrpTyr 180 2230 TATTGTACAACTGGGTCTCTGTGAGCGAAACTTCAGAAGTTTATCAGCAAGC 2283	181	190 sLysLeulleGluArgMetValArgThrAspSetLeuTrpAr 204	204 gGlyLeuAlaGluArgArgGlyTrpGlyGlnTyrLeuPheLysAsnLysProProAspGl 224 2398 2398	224 yAsnAlaProProAsnSerPheTytArgAlaLeuTyrProLysIleIleGlnAspIleGl 244 2399GAGGATGGTCA 2427	244 uThrileGluSerAenTrpArgCysGlyArgHisSerLeuGlnArg1leHisCysArgSe 264 : ::::: 2428 GAGAATAGCTTCTTGTGGAGCTGATAAACCTTACAGGTGTTCAAAGC 2475	264 rGluThrSerLys	274 nTyrAspaspGlnLyslleValSerGlyLeuargaspasnThrIleLyslleTr 292

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8 8 8 8 8 8 8 8	868686868	6 8 6 8 6 8 6 8 6	8 3 8 3 8 3 8 3
QY   511 sLeuArgThrLeuValGluHisSerGlyArgValPheArgLeuGlnPheAspGl 529   1	SS: SS: SS: SS: SS: SS: SS: SS: SS: SS:	APPLICATION NUMBER: 60/055,258 FILING DATE: 07-AUG-1997 ATTORNEY/AGENT INFORMATION: NAME: Kettelberger, Ph.D., Denise M REGISTRATION NUMBER: 33,924 REFERENCE/DOCKET NUMBER: 11669.6USUI TELECOMMUNICATION INFORMATION: TELEX: 12-332-9081 TELEX: 612-332-9081 TELEX: 612-332-9081 TELEX: 100-322-9081 TREE: 100-322-9081 TYPE: 100-322-322-9081 TYPE: 100-322-322-9081 TYPE: 100-322-322-322-322-322-322-322-322-322-3	Alignment Scores:   1.6e-23   Length: 7075     Pred. No.:   299.50   Matches: 154     Score:   33.77\$   Matches: 154     Best Local Similarity:   33.77\$   Conservative: 102     Best Local Similarity:   20.32\$   Mismatches:   195     Query Match:   3.87\$   Indels:   308     US-09-601-168B-2 (1-569) x US-09-092-508-15 (1-7075)     Qy

us-09-601-168b-2.rni

2689 CTGCCATTTCACCAACAGTAGTCATCTTCTTTAGCCACTGGGTCAAGTGACTGCTT 2748

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1850 TTCTGTGATCGAATGGAAGTCGTTTCGTTATTATTTACATGATCTTCAAGTAGATTTT 1909
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                                                                                                                                                                               ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6346607west Center, 90 South Seventh St
CITY: Minneapolis
                 Sequence 15, Application US/09435115
Patent No. 6346607
GENERAL INFORMATION:
APPLICANT: Henzel, William J.
TITLE OF INVENTION: APAP-1, AN ACTIVATOR OF C ASPASE-3
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7075
154
102
195
308
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM.

OPERATING SYSTEM.

SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/435,115
FILING DATE:
CLASSIFFCATION:
PRICATION NUMBER: 09/092,508
FILING DATE:
APPLICATION NUMBER: 60/055,258
FILING DATE:
APPLICATION NUMBER: 07-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-601-168B-2 (1-569) x US-09-435-115-15 (1-7075)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1802 GAAGAAGTTGAAGACATACTGCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kettelberger, Ph.D., I
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Coding Sequence
LOCATION: 578...4192
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                          COMPUTER ENABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.6e-23
299.50
33.77%
20.32%
9.87%
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SEQUENCE CHARACTERISTICS:
LENGTH: 7075 base pairs
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                             USA
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US-09-435-115-15
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                                                                                                                                                                                                                                                    STATE: M
COUNTRY:
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                                                                                                                                     2868
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3409 TTTAGAACTIGTAAACAATAGAATCTTCCAGTCCAGGTTTCAGCACAAGAAACTGTATG 3468
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                                                                                                                                                                                                                           8869 TGGAACCTTAAAGCTTTGGGATGCGACATCAGCAAATGAGAGAAAAGCATTAATGTGAA 2928
                                                                                                                                                                                                                                                                                                                         2929 ACAGTICTICCIAAAIITGGAGGACCCICAAGAGGATAIGGAAGIGAIAGIGAAGIGIIG 2988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1049 GAATACAGACTCACGTTCAAAGGTGGCTGATTGCAGAGGACATTTAAGTTGGGTTCATGG 3108
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                                                                                                                                                                               pargserilealaValTrpAspMetAlaSerProThrAsp------IleThrLeuAr 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------GlyHisArgAlaAlaValAsnVa 395
                                                                                                                         2809 ITCAGTCAATCACTGCAGATTTTCACCAGATGATAAGCTTTTGGCTAGTTGTTCAGCTGA
                                         2749 CCTCAAACTTTGGGATTTGAATCAAAAGAATGTCGAAATACCATGTTTGGTCATACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                434 aCysLeuGlnTyrArg-----AspArgLeuValValSerGlySerSerAspAsnThril
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      472 uValArgCysIleArg---PheAspAsnLysArgIleValSerGlyAlaTyrAspGlyLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               491 sileLysvalTrpAspLeuValAlaAlaLeuAspProArgAlaProAlaGlyThrLeuCy
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328 rValArgValTrpAspValAsnThrGlyGluMetLeuAsnThrLeuIleHisHisCysGl
                                                                                      348 uAlaValLeuHisLeuArgPhe-----AsnAsnGlyMetMetValThrCysSerLysAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :::||||||||||3646 AGTAATATTATTACTGGAAATAAAGAA-----
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uAlaSe 61 ::::: TGGTAC 2029  rSerSe 81  rSerSe 81  reduCy 101	Ly 190 ACAA 2376 FPAR 204 2431 SpG1 224 2431 IeG1 244 iii 2460 FG26 264 FG17 274 GTGC 2568 euG1 274 GTGC 2568 euG1 274 GTGC 2568 GTT 2748 GTTG 2688 erTh 328 GTT 2748 ysG1 348
42 GINThrTyrAsnSerCysAlaArgLeuCysLeuAsnGlnGlu-ThrValCysLeuAlaSe [	TAAGCTGCAGGCCAAGGAGGTCGATAATGGAATGCTTTACCTGGA slysLeulleGluargMetValArgThras slysLeulleGluargMetValArg

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1507 TATTTTGTGTCAGGGGCCATGACCGAGTAGCTCGGCTCTGGGCTACAGACCACTATCAG 1566
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                                                                                                                                                                                                                                  LeuThrGlyHisThrGlySerValLeuCysLeuGlnTyr-----AspGluArgVallle 320
                                                                                                                                                                                                                                                                                                                                                                                                341 AsnThrLeulleHisHisCysGluAlaValLeuHisLeuArgPheAsn-----AsnGly 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359 MetMetValThrCysSerLysAspArgSerIleAlaValTrp-----AspMetAlaSer 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415 TrpAsnThrSerThrCysGluPheValArgThrLeuAsnGlyHisLysArgGlyIleAla 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---ArgAlaProAlaGlyThr-----LeuCysLeuArgThrLeu 515
                                                                                                                                                                                         1267 GAATCAGATGTCTTAGAAAGAATCATGGÁTGAGAAAÁCAGCAAGTGAGTTGAAGÁTT
                                                                                                                                                                                                                                                                                                                                        1447 GTGGGATATAAAGGACÁCAACTATCCAGTATGGGACACACAATTTTCTCCATATGGATAT
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                                                                                                                                                  AsplysAsnThrLeuGluCysLysArgile
                                                                                                                                                                                                                                                                                                                  321 IleThrGlySerSerAspSerThrValArgValTrpAspValAsnThrGlyGluMetLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProThrAsplleThrLeuArgArgValLeuValGlyHisArgAlaAlaValAsnValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            397 AspPhe-----AspAspLysTyrIleValSerAlaSerGlyAspArgThr11eLysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     453 ArgieuTrpAsplleGluCysGlyAlaCysLeuArgValLeuGluGlyHisGluGluLeu
                                                                                                              GTAACACCCAAAAAGCTTCGTAGTGTCAAACAAGCATCAGATCTTAGTTGTATAGACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 491 LysIleLysValTrpAspLeuValAlaAlaLeuAspPro-------------
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Job time : 149 secs
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APPLICANT: Comai, Lucio
APPLICANT: Pynlact, Brian D.
APPLICANT: Hoey, Timethy Timethy
APPLICANT: Ruppert, Siegfried
APPLICANT: Tanese, Nacko
APPLICANT: Wang, Edith
APPLICANT: Wang, Edith
APPLICANT: Wang, Edith
APPLICANT: Waltzierl, Robert O.J.
APPLICANT: Waltzierl, Robert O.J.
APPLICANT: Waltzierl, Nucleuc O.J.
APPLICANT: Waltzierl, Nucleuc Acids Encoding Tafs AND METHODS OF USE
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
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100
54
143
101
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COMPUTER: IR PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,582
FILING DATE: 28-JAN-1994
CLASSIFICATION: 43-6
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
TELEFONE: (415) 781-1989
TELEFONE: (415) 781-1989
TELEFX: 910 277299
INPORMATION FOR INFORMATION:
TELEFX: 910 277299
INPORMATION FOR SEQ ID NO: 17:
SEQUENCE CHRAACTERISTICS:
FUNNEME: Asse Dairs
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                           ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: double
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38,69%
25,13%
9,84%
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LOCATION: 1....
iS-08-188-582-17
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